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OM protein - protein search, using sw model

Run on: May 10, 2005, 18:26:54 ; Search time 167 Seconds
(without alignments)
592.878 Million cell updates/sec

Title: US-09-785-019B-335
Perfect score: 1444
Sequence: 1 MQHHHHHHGSDVRDLNALLP.....TSQLECMTWNQMNLGATLKG 256

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1444	100.0	256	5	ABG33384	Abg33384 Human WT1
2	1444	100.0	256	7	ADB67537	Adb67537 Human Wil
3	1444	100.0	256	7	ADJ80770	Adj80770 Wilm's tu
4	1444	100.0	256	8	ADJ83690	Adj83690 Human WT1
5	1444	100.0	256	8	ADL57578	Adl57578 Human WT-
6	1444	100.0	256	8	ADO09133	Ado09133 Human WT1
7	1418.5	98.2	410	5	ABG33382	Abg33382 Human Trx
8	1418.5	98.2	410	7	ADB67535	Adb67535 Human WT1
9	1418.5	98.2	410	7	ADJ80768	Adj80768 Wilm's tu
10	1418.5	98.2	410	8	ADJ83688	Adj83688 Human WT1
11	1418.5	98.2	410	8	ADL57576	Adl57576 Human Trx
12	1418.5	98.2	410	8	ADO09131	Ado09131 Human Trx
13	1418	98.2	591	5	ABG33383	Abg33383 Human Trx
14	1418	98.2	591	7	ADB67536	Adb67536 Human WT1
15	1418	98.2	591	7	ADJ80769	Adj80769 Wilm's tu
16	1418	98.2	591	8	ADJ83689	Adj83689 Human WT1
17	1418	98.2	591	8	ADL57577	Adl57577 Human Trx
18	1418	98.2	591	8	ADO09132	Ado09132 Human Trx
19	1394	96.5	292	7	ADJ80934	Adj80934 Wilm's tu
20	1394	96.5	292	7	ADJ80905	Adj80905 Wilm's tu
21	1394	96.5	292	8	ADL57713	Adl57713 Human TAT
22	1394	96.5	292	8	ADL57742	Adl57742 Human TAT
23	1394	96.5	292	8	ADO09268	Ado09268 pStumpy-W
24	1394	96.5	292	8	ADO09297	Ado09297 pStumpy-W
25	1394	96.5	321	7	ADJ80914	Adj80914 Wilm's tu
26	1394	96.5	321	7	ADJ80890	Adj80890 Wilm's tu
27	1394	96.5	321	8	ADJ83810	Adj83810 Human WT1
28	1394	96.5	321	8	ADL57698	Adl57698 Human Wil
29	1394	96.5	321	8	ADL57722	Adl57722 Human TAT
30	1394	96.5	321	8	ADO09253	Ado09253 Human WT1
31	1394	96.5	321	8	ADO09277	Ado09277 Codon opt
32	1394	96.5	469	7	ADJ80889	Adj80889 Wilm's tu
33	1394	96.5	469	8	ADJ83809	Adj83809 Human WT1
34	1394	96.5	469	8	ADL57697	Adl57697 Human Wil
35	1394	96.5	469	8	ADO09252	Ado09252 Human WT-
36	1386	96.0	280	7	ADJ80896	Adj80896 Wilm's tu
37	1386	96.0	280	8	ADJ83816	Adj83816 Human WT1
38	1386	96.0	280	8	ADL57704	Adl57704 Human Wil
39	1386	96.0	280	8	ADO09259	Ado09259 Human WT-
40	1386	96.0	281	7	ADJ80900	Adj80900 Wilm's tu
41	1386	96.0	281	8	ADJ83820	Adj83820 Recombina
42	1386	96.0	281	8	ADL57708	Adl57708 Human WT-
43	1386	96.0	281	8	ADO09263	Ado09263 Human WT-
44	1386	96.0	291	7	ADJ80899	Adj80899 Wilm's tu
45	1386	96.0	291	8	ADJ83819	Adj83819 Recombina

ALIGNMENTS

RESULT 1
ABG33384
ID ABG33384 standard; protein; 256 AA.
XX
AC ABG33384;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human WT1-A.
XX
KW Human; mouse; cytostatic; immunostimulant; WT1; cancer; immune response.
XX
OS Homo sapiens.
XX
PN WO200228414-A1.
XX
PD 11-APR-2002.
XX
PF 03-OCT-2001; 2001WO-US031139.
XX
PR 06-OCT-2000; 2000US-00684361.
PR 09-OCT-2000; 2000US-00685830.
PR 15-FEB-2001; 2001US-00785019.
PR 24-AUG-2001; 2001US-00938864.
XX
PA (CORI-) CORIXA CORP.
PA (GAIG/) GAIGER A.
XX
PI Gaiger A, Mcneill PD, Smithgall M, Moulton G, Vedvick TS;
PI Sleath PR, Mossman S, Evans L, Spies AG, Boydston J;
XX
DR WPI; 2002-352217/38.
DR N-PSDB; ABK69666.
XX
PT Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for
PT treating and diagnosing cancer in a patient.
XX
PS Claim 2; Page 223-224; 260pp; English.
XX
CC The invention relates to an isolated WT1 polynucleotide (I) and
CC polypeptide encoded by (I). The WT1 polynucleotides and polypeptides are
CC used for treating and detecting cancer in a patient, and for stimulating
CC an immune response in patient. ABG33070-ABG33405 represent WT1 amino acid
CC sequences of the invention
XX
SQ Sequence 256 AA;

Query Match 100.0%; Score 1444; DB 5; Length 256;

```
  Best Local Similarity   100.0%;  Pred. No. 2.2e-104;
  Matches  256;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MQHHHHHHGSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MQHHHHHHGSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGG 60

Qy         61 PAPPPAPPPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PAPPPAPPPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFG 120

Qy        121 PPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPN 180

Qy        181 HSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQL 240

Qy        241 ECMTWNQMNLGATLKG 256
              ||||||||||||||||
Db        241 ECMTWNQMNLGATLKG 256


RESULT 2
ADB67537
ID   ADB67537 standard; protein; 256 AA.
XX
AC   ADB67537;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human Wilm's tumour protein, WT1A.
XX
KW   Human; Wilm's tumour antigen; WT1; cytostatic; antigen; T cell;
KW   antigen-presenting cell; CD4+; CD8+; immune response; cancer; vaccine;
KW   leukaemia; antigen.
XX
OS   Homo sapiens.
XX
PN   US2003072767-A1.
XX
PD   17-APR-2003.
XX
PF   24-AUG-2001; 2001US-00938864.
XX
PR   30-SEP-1998;   98US-00164223.
PR   25-MAR-1999;   99US-00276484.
PR   06-OCT-2000; 2000US-00684361.
PR   09-OCT-2000; 2000US-00685830.
PR   15-FEB-2001; 2001US-00785019.
XX
PA   (GAIG/) GAIGER A.
PA   (MCNE/) MCNEILL P D.
PA   (SMIT/) SMITHGALL M.
PA   (MOUL/) MOULTON G.
PA   (VEDV/) VEDVICK T S.
PA   (SLEA/) SLEATH P R.
PA   (MOSS/) MOSSMAN S.
PA   (EVAN/) EVANS L.
PA   (SPIE/) SPIES A G.
PA   (BOYD/) BOYDSTON J.
XX
PI   Gaiger A,  Mcneill PD,  Smithgall M,  Moulton G,  Vedvick TS;
PI   Sleath PR,  Mossman S,  Evans L,  Spies AG,  Boydston J;
XX
DR   WPI; 2003-605957/57.
DR   N-PSDB; ADB67532.
XX
PT   Novel Wilms tumor polynucleotides encoding WT1 polypeptides, useful for
PT   detecting the presence of cancer in a patient, and in pharmaceutical
PT   compositions, e.g. vaccines, for treating cancers e.g. leukemia.
XX
PS   Claim 2; Page 127; 197pp; English.
XX
CC   The invention relates to an isolated Wilm tumour (WT1) polynucleotide
CC   comprising a full length protein, truncated protein, mutated protein or
CC   fusion protein. Also included are the encoded WT1 proteins, expression
CC   vectors, host cells, antibodies, detecting the presence of a cancer in a
CC   patient by contacting a biological sample with a binding agent that binds
CC   to a WT1 protein, an oligonucleotide that hybridises to a WT1
CC   polynucleotide, stimulating and/or expanding T cells specific for a
CC   tumour protein by contacting T cells with the WT1 polynucleotide, the WT1
CC   protein or antigen-presenting cells that express the WT1 protein, a
CC   composition (C1) (comprising physiologically acceptable carriers and
CC   immunostimulants as first component, and a second component selected from
CC   the WT1 polynucleotide, the WT1 protein, Ab, or T cells and antigen
CC   presenting cells that express the WT1 protein), inhibiting the
CC   development of a cancer in a patient (by incubating CD4+ and/or CD8+ T
CC   cells isolated from a patient with the WT1 polynucleotide, the WT1
CC   protein or antigen presenting cells that express the WT1 protein, such
CC   that T cell proliferate, administering the proliferated T cells to the
CC   patient, and thus inhibiting the development of a cancer in the patient)
CC   and a composition (C2) (comprising a WT1 polypeptide resuspended in a
CC   buffer comprising at least 1-3 sugars selected from trehalose, maltose,
CC   sucrose, fructose and glucose, at a concentration of 7-13%, and
CC   optionally ethanolamine, cysteine and Polysorbate-80, or WT1 polypeptide
CC   and MPL-SE or Enhanzyn). Also disclosed as anew are polypeptides
CC   comprising a variant of an immunogenic portion of WT1 polypeptide. C1 is
CC   useful for stimulating immune response in a patient, and for treating
CC   cancer in a patient. The oligonucleotide is also useful for determining
CC   the presence of a cancer in a patient. The WT1 polynucleotide and the WT1
CC   protein are useful in pharmaceutical compositions, e.g. vaccines. the WT1
CC   protein is useful as marker to indicate the presence or absence of a
CC   cancer. C1 is useful for inhibiting the development of a malignant
CC   disease in a patient, for preventing and treating metastatic diseases
CC   e.g. leukaemia and cancer, and for removing tumour cells from a
CC   biological sample. Ab (binding agent for the WT1 protein) is useful for
CC   detecting the presence of cancer in a patient. The present sequence is
CC   the Human Wilm's tumour gene product, WT1 protein.
XX
SQ   Sequence 256 AA;

  Query Match             100.0%;  Score 1444;  DB 7;  Length 256;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-104;
  Matches  256;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MQHHHHHHGSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MQHHHHHHGSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGG 60

Qy         61 PAPPPAPPPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PAPPPAPPPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFG 120

Qy        121 PPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPN 180

Qy        181 HSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQL 240

Qy        241 ECMTWNQMNLGATLKG 256
              ||||||||||||||||
Db        241 ECMTWNQMNLGATLKG 256


RESULT 3
ADJ80770
ID   ADJ80770 standard; protein; 256 AA.
XX
AC   ADJ80770;
XX
DT   06-MAY-2004  (first entry)
XX
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```
DE   Wilm's tumor antigen associated protein #4.
XX
KW   cytostatic; gene therapy; vaccine; Wilm's tumor antigen; WT1; cancer;
KW   leukemia.
XX
OS   Homo sapiens.
XX
PN   WO2003037060-A2.
XX
PD   08-MAY-2003.
XX
PF   30-OCT-2002; 2002WO-US035194.
XX
PR   30-OCT-2001; 2001US-00002603.
PR   16-APR-2002; 2002US-00125635.
PR   12-JUL-2002; 2002US-00195835.
PR   16-SEP-2002; 2002US-00244830.
XX
PA   (CORI-) CORIXA CORP.
PA   (GAIG/) GAIGER A.
XX
PI   Gaiger A,  Mcneill PD,  Jaya N,  Carter D;
XX
DR   WPI; 2003-430453/40.
XX
PT   New isolated polypeptide for diagnosing, preventing or treating malignant
PT   diseases, e.g. cancer or leukemia, comprises an immunogenic portion of a
PT   Wilms' tumor antigen.
XX
PS   Disclosure; SEQ ID NO 335; 371pp; English.
XX
CC   The invention relates to an isolated polypeptide comprising an
CC   immunogenic portion of a Wilm's tumor antigen, or its variant that
CC   differs in one or more substitutions, deletions, additions and/or
CC   insertions, such that the ability of the variant to react with WT1-
CC   specific antisera and/or T-cell lines or clones is not substantially
CC   diminished. The composition and methods are useful in diagnosing,
CC   preventing or treating malignant diseases, such as cancer or leukemia.
CC   This sequence represents a protein of the invention.
XX
SQ   Sequence 256 AA;

  Query Match             100.0%;  Score 1444;  DB 7;  Length 256;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-104;
  Matches  256;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MQHHHHHHGSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MQHHHHHHGSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGG 60

Qy         61 PAPPPAPPPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PAPPPAPPPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFG 120

Qy        121 PPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPN 180

Qy        181 HSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQL 240

Qy        241 ECMTWNQMNLGATLKG 256
              ||||||||||||||||
Db        241 ECMTWNQMNLGATLKG 256


RESULT 4
ADJ83690
ID   ADJ83690 standard; protein; 256 AA.
XX
AC   ADJ83690;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human WT1 (Wilms tumour)-related WT1_A protein.
XX
KW   immune response; WT1; Wilms tumour; immunostimulant; cytostatic; vaccine;
KW   malignant disease; leukaemia; cancer; human; WT1_A.
XX
OS   Homo sapiens.
XX
PN   US2003235557-A1.
XX
PD   25-DEC-2003.
XX
PF   16-SEP-2002; 2002US-00244830.
XX
PR   30-SEP-1998;   98US-00164223.
PR   25-MAR-1999;   99US-00276484.
PR   06-OCT-2000; 2000US-00684361.
PR   09-OCT-2000; 2000US-00685830.
PR   15-FEB-2001; 2001US-00785019.
PR   24-AUG-2001; 2001US-00938864.
PR   30-OCT-2001; 2001US-00002603.
PR   16-APR-2002; 2002US-00125635.
PR   12-JUL-2002; 2002US-00195835.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Gaiger A,  Cheever MA;
XX
DR   WPI; 2004-070542/07.
DR   N-PSDB; ADJ83685.
XX
PT   Inducing an immune response in an animal, useful for treating or
PT   preventing cancer, comprises administering a composition comprising a
PT   viral vector comprising an immunogenic portion of a WT1 polynucleotide.
XX
PS   Example 9; SEQ ID NO 335; 229pp; English.
XX
CC   The invention relates to a novel method for inducing an immune response
CC   in an animal which involves administering a first and a second
CC   composition comprising a first and a second viral vector, respectively,
CC   each having at least an immunogenic portion of a WT1 (Wilms tumour)
CC   polynucleotide operably linked to an expression control sequence. The
CC   method of the invention has immunostimulant and cytostatic applications
CC   and may be useful for generating or enhancing an immune response to WT1,
CC   possibly via the production of a vaccine, as well as for preventing
CC   and/or treating malignant diseases such as leukaemia and cancer. The
CC   current sequence is that of the human WT1-related protein of the
CC   invention.
XX
SQ   Sequence 256 AA;

  Query Match             100.0%;  Score 1444;  DB 8;  Length 256;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-104;
  Matches  256;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MQHHHHHHGSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MQHHHHHHGSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGG 60

Qy         61 PAPPPAPPPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PAPPPAPPPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFG 120

Qy        121 PPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPN 180

Qy        181 HSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQL 240

Qy        241 ECMTWNQMNLGATLKG 256
```

```
                ||||||||||||||||
Db        241 ECMTWNQMNLGATLKG 256


RESULT 5
ADL57578
ID   ADL57578 standard; protein; 256 AA.
XX
AC   ADL57578;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Human WT-1 N-terminal open reading frame, WT-1A.
XX
KW   Human; Wilms' tumour; WT1; cancer; cytostatic; immunogen; antigen;
KW   vaccine; T-cell; MHC; Major Histocompatibility Complex; HLA-A2;
KW   human leukocyte antigen; Ra12; HIS tag; twin arginine translocator; TAT;
KW   malignant disease; mutein; mutant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US2003215458-A1.
XX
PD   20-NOV-2003.
XX
PF   30-OCT-2002; 2002US-00286333.
XX
PR   30-SEP-1998;   98US-00164223.
PR   25-MAR-1999;   99US-00276484.
PR   06-OCT-2000; 2000US-00684361.
PR   09-OCT-2000; 2000US-00685830.
PR   15-FEB-2001; 2001US-00785019.
PR   24-AUG-2001; 2001US-00938864.
PR   30-OCT-2001; 2001US-00002603.
PR   16-APR-2002; 2002US-00125635.
PR   12-JUL-2002; 2002US-00195835.
PR   16-SEP-2002; 2002US-00244830.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Gaiger A,  Mcneill PD,  Jaya N;
XX
DR   WPI; 2004-021827/02.
DR   N-PSDB; ADL57573.
XX
PT   New polypeptides and polynucleotides useful for generating or enhancing
PT   an immune response to Wilms' tumor, or for treating and/or preventing
PT   malignant diseases, e.g. cancer.
XX
PS   Example 9; SEQ ID NO 335; 259pp; English.
XX
CC   The invention relates to an isolated polypeptide comprising an
CC   immunogenic portion of a Wilms' tumour antigen (WT1), or their variants
CC   that differs in substitution(s), deletion(s), addition(s) and/or
CC   insertion(s), where ability of the variant to react with WT1-specific
CC   antisera and/or T-cell lines or clones is not substantially diminished.
CC   Also included are a fusion protein comprising at least one WT1
CC   polypeptide, an isolated polynucleotide encoding the fusion protein, a
CC   composition comprising a WT1 polypeptide in combination with a
CC   pharmaceutical carrier or excipient, a vaccine comprising a WT1
CC   polypeptide in combination with a non-specific immune response enhancer,
CC   an expression vector comprising the polynucleotide operably linked to an
CC   expression control sequence and a host cell transformed or transfected
CC   with the expression vector. The immunogenic portion of the WT1
CC   polypeptide has been modified such that the ability of the immunogenic
CC   portion to bind to an MHC (Major Histocompatibility Complex) molecule or
CC   to HLA-A2 is increased relative to that of the immunogenic portion. The
CC   WT1 polypeptide may comprise a Wilms' tumour antigen having a deletion of
CC   a proline rich region at amino acid positions 54-68 of the Wilms' tumour
CC   antigen. The fusion partner is selected from Ra12, protein D, LYTA, a HIS
CC   tag, a targeting signal capable of directing a polypeptide to the
CC   endosomal/lysosomal compartment, twin arginine translocator (TAT), and
CC   truncated twin arginine translocator. The polypeptide, polynucleotide or
CC   compositions comprising them may be used for generating or enhancing an
CC   immune response to Wilms' tumour, and for treating and/or preventing
CC   malignant diseases, e.g. cancer. The compositions may be used as markers
CC   for the progression of cancer. The present sequence is a mutated or
CC   truncated WT-1 protein.
XX
SQ   Sequence 256 AA;

  Query Match           100.0%;  Score 1444;  DB 8;  Length 256;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-104;
  Matches  256;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MQHHHHHHGSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MQHHHHHHGSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGG 60

Qy         61 PAPPPAPPPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PAPPPAPPPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFG 120

Qy        121 PPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPN 180

Qy        181 HSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQL 240

Qy        241 ECMTWNQMNLGATLKG 256
              ||||||||||||||||
Db        241 ECMTWNQMNLGATLKG 256


RESULT 6
ADO09133
ID   ADO09133 standard; protein; 256 AA.
XX
AC   ADO09133;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human WT1_A.
XX
KW   Wilms' tumour antigen; WT1; vaccine; malignant disease; immunogenic;
KW   leukaemia; cancer; human.
XX
OS   Homo sapiens.
XX
PN   US2004018204-A1.
XX
PD   29-JAN-2004.
XX
PF   30-APR-2003; 2003US-00427717.
XX
PR   24-AUG-2001; 2001US-00938864.
PR   30-OCT-2001; 2001US-00002603.
PR   16-APR-2002; 2002US-00125635.
PR   12-JUL-2002; 2002US-00195835.
PR   16-SEP-2002; 2002US-00244830.
PR   30-OCT-2002; 2002US-00286333.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Gaiger A,  Mcneill PD,  Jaya N;
XX
DR   WPI; 2004-121992/12.
DR   N-PSDB; ADO09128.
XX
PT   New polypeptides and polynucleotides comprising an immunogenic portion of
PT   a Wilms' tumor antigen, useful as vaccines for preventing or treating
PT   malignant diseases, e.g. cancer or leukemia.
XX
```

```
PS   Example 9; SEQ ID NO 335; 252pp; English.
XX
CC   The invention relates to an isolated polypeptide which comprises an
CC   immunogenic portion of a Wilms' tumour antigen having a deletion of a
CC   proline rich region, so that the ability of the variant to react with WT1
CC   -specific antisera and/or T-cell lines or clones is not substantially
CC   diminished. The polypeptide is useful as a vaccine in combination with a
CC   non-specific immune response enhancer for preventing malignant diseases.
CC   The polypeptide is useful for enhancing or inducing an immune response in
CC   a patient; for inhibiting the development of malignant disease in a
CC   patient; for stimulating or expanding T cells. The polypeptides,
CC   polynucleotides and compositions are useful for treating malignant
CC   diseases including leukaemia and cancer. The present sequence represents
CC   the amino acid sequence of a human WT1.
XX
SQ   Sequence 256 AA;

  Query Match             100.0%;  Score 1444;  DB 8;  Length 256;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-104;
  Matches  256;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MQHHHHHHHGSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MQHHHHHHHGSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGG 60

Qy         61 PAPPPAPPPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PAPPPAPPPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFG 120

Qy        121 PPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPN 180

Qy        181 HSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQL 240

Qy        241 ECMTWNQMNLGATLKG 256
              ||||||||||||||||
Db        241 ECMTWNQMNLGATLKG 256


RESULT 7
ABG33382
ID   ABG33382 standard; protein; 410 AA.
XX
AC   ABG33382;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Human Trx_WT1_A.
XX
KW   Human; mouse; cytostatic; immunostimulant; WT1; cancer; immune response.
XX
OS   Homo sapiens.
XX
PN   WO200228414-A1.
XX
PD   11-APR-2002.
XX
PF   03-OCT-2001; 2001WO-US031139.
XX
PR   06-OCT-2000; 2000US-00684361.
PR   09-OCT-2000; 2000US-00685830.
PR   15-FEB-2001; 2001US-00785019.
PR   24-AUG-2001; 2001US-00938864.
XX
PA   (CORI-) CORIXA CORP.
PA   (GAIG/) GAIGER A.
XX
PI   Gaiger A,  Mcneill PD,  Smithgall M,  Moulton G,  Vedvick TS;
PI   Sleath PR,  Mossman S,  Evans L,  Spies AG,  Boydston J;
XX
DR   WPI; 2002-352217/38.
DR   N-PSDB; ABK69664.
XX
PT   Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for
PT   treating and diagnosing cancer in a patient.
XX
PS   Claim 2; Page 221-222; 260pp; English.
XX
CC   The invention relates to an isolated WT1 polynucleotide (I) and
CC   polypeptide encoded by (I). The WT1 polynucleotides and polypeptides are
CC   used for treating and detecting cancer in a patient, and for stimulating
CC   an immune response in patient. ABG33070-ABG33405 represent WT1 amino acid
CC   sequences of the invention
XX
SQ   Sequence 410 AA;

  Query Match             98.2%;  Score 1418.5;  DB 5;  Length 410;
  Best Local Similarity   89.2%;  Pred. No. 3.5e-102;
  Matches  256;  Conservative    0;  Mismatches    0;  Indels   31;  Gaps    1;

Qy          1 MQHHHHHH------------------------------GSDVRDLNALLPAVPSLGGGG 29
              ||||||||                              ||||||||||||||||||||
Db        124 MQHHHHHHVSIEGRASSGGSGLVPRGSSGSGDDDDKSSRGSDVRDLNALLPAVPSLGGGG 183

Qy         30 GCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPPPPPPPPPHSFIKQEPSWGGAE 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPPPPPPPPPHSFIKQEPSWGGAE 243

Qy         90 PHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQP 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 PHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQP 303

Qy        150 AIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYGC 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 AIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYGC 363

Qy        210 HTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQMNLGATLKG 256
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 HTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQMNLGATLKG 410


RESULT 8
ADB67535
ID   ADB67535 standard; protein; 410 AA.
XX
AC   ADB67535;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human WT1-A-Trx fusion protein.
XX
KW   Human; Wilm's tumour antigen; WT1; cytostatic; antigen; T cell;
KW   antigen-presenting cell; CD4+; CD8+; immune response; cancer; vaccine;
KW   leukaemia; antigen.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US2003072767-A1.
XX
PD   17-APR-2003.
XX
PF   24-AUG-2001; 2001US-00938864.
XX
PR   30-SEP-1998;   98US-00164223.
PR   25-MAR-1999;   99US-00276484.
PR   06-OCT-2000; 2000US-00684361.
PR   09-OCT-2000; 2000US-00685830.
PR   15-FEB-2001; 2001US-00785019.
XX
PA   (GAIG/) GAIGER A.
PA   (MCNE/) MCNEILL P D.
PA   (SMIT/) SMITHGALL M.
```

PA (MOUL/) MOULTON G.
PA (VEDV/) VEDVICK T S.
PA (SLEA/) SLEATH P R.
PA (MOSS/) MOSSMAN S.
PA (EVAN/) EVANS L.
PA (SPIE/) SPIES A G.
PA (BOYD/) BOYDSTON J.
XX
PI Gaiger A, Mcneill PD, Smithgall M, Moulton G, Vedvick TS;
PI Sleath PR, Mossman S, Evans L, Spies AG, Boydston J;
XX
DR WPI; 2003-605957/57.
DR N-PSDB; ADB67530.
XX
PT Novel Wilms tumor polynucleotides encoding WT1 polypeptides, useful for
PT detecting the presence of cancer in a patient, and in pharmaceutical
PT compositions, e.g. vaccines, for treating cancers e.g. leukemia.
XX
PS Claim 2; Page 124-125; 197pp; English.
XX
CC The invention relates to an isolated Wilm tumour (WT1) polynucleotide
CC comprising a full length protein, truncated protein, mutated protein or
CC fusion protein. Also included are the encoded WT1 proteins, expression
CC vectors, host cells, antibodies, detecting the presence of a cancer in a
CC patient by contacting a biological sample with a binding agent that binds
CC to a WT1 protein, an oligonucleotide that hybridises to a WT1
CC polynucleotide, stimulating and/or expanding T cells specific for a
CC tumour protein by contacting T cells with the WT1 polynucleotide, the WT1
CC protein or antigen-presenting cells that express the WT1 protein, a
CC composition (C1) (comprising physiologically acceptable carriers and
CC immunostimulants as first component, and a second component selected from
CC the WT1 polynucleotide, the WT1 protein, Ab, or T cells and antigen
CC presenting cells that express the WT1 protein), inhibiting the
CC development of a cancer in a patient (by incubating CD4+ and/or CD8+ T
CC cells isolated from a patient with the WT1 polynucleotide, the WT1
CC protein or antigen presenting cells that express the WT1 protein, such
CC that T cell proliferate, administering the proliferated T cells to the
CC patient, and thus inhibiting the development of a cancer in the patient)
CC and a composition (C2) (comprising a WT1 polypeptide resuspended in a
CC buffer comprising at least 1-3 sugars selected from trehalose, maltose,
CC sucrose, fructose and glucose, at a concentration of 7-13%, and
CC optionally ethanolamine, cysteine and Polysorbate-80, or WT1 polypeptide
CC and MPL-SE or Enhanzyn). Also disclosed as anew are polypeptides
CC comprising a variant of an immunogenic portion of WT1 polypeptide. C1 is
CC useful for stimulating immune response in a patient, and for treating
CC cancer in a patient. The oligonucleotide is also useful for determining
CC the presence of a cancer in a patient. The WT1 polynucleotide and the WT1
CC protein are useful in pharmaceutical compositions, e.g. vaccines. the WT1
CC protein is useful as marker to indicate the presence or absence of a
CC cancer. C1 is useful for inhibiting the development of a malignant
CC disease in a patient, for preventing and treating metastatic diseases
CC e.g. leukaemia and cancer, and for removing tumour cells from a
CC biological sample. Ab (binding agent for the WT1 protein) is useful for
CC detecting the presence of cancer in a patient. The present sequence
CC represents a Human WT1 fusion protein.
XX
SQ Sequence 410 AA;

```
  Query Match             98.2%;  Score 1418.5;  DB 7;  Length 410;
  Best Local Similarity   89.2%;  Pred. No. 3.5e-102;
  Matches  256;  Conservative    0;  Mismatches    0;  Indels   31;  Gaps    1;

Qy          1 MQHHHHHH----------------------------GSDVRDLNALLPAVPSLGGGG 29
              ||||||||                            |||||||||||||||||||||
Db        124 MQHHHHHHVSIEGRASSGGSGLVPRGSSGSGDDDDKSSRGSDVRDLNALLPAVPSLGGGG 183

Qy         30 GCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPPPPPPPPPHSFIKQEPSWGGAE 89
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPPPPPPPPPHSFIKQEPSWGGAE 243

Qy         90 PHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQP 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 PHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQP 303

Qy        150 AIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYGC 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 AIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYGC 363

Qy        210 HTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQMNLGATLKG 256
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 HTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQMNLGATLKG 410
```

RESULT 9
ADJ80768
ID ADJ80768 standard; protein; 410 AA.
XX
AC ADJ80768;
XX
DT 06-MAY-2004 (first entry)
XX
DE Wilm's tumor antigen associated protein #2.
XX
KW cytostatic; gene therapy; vaccine; Wilm's tumor antigen; WT1; cancer;
KW leukemia.
XX
OS Homo sapiens.
XX
PN WO2003037060-A2.
XX
PD 08-MAY-2003.
XX
PF 30-OCT-2002; 2002WO-US035194.
XX
PR 30-OCT-2001; 2001US-00002603.
PR 16-APR-2002; 2002US-00125635.
PR 12-JUL-2002; 2002US-00195835.
PR 16-SEP-2002; 2002US-00244830.
XX
PA (CORI-) CORIXA CORP.
PA (GAIG/) GAIGER A.
XX
PI Gaiger A, Mcneill PD, Jaya N, Carter D;
XX
DR WPI; 2003-430453/40.
XX
PT New isolated polypeptide for diagnosing, preventing or treating malignant
PT diseases, e.g. cancer or leukemia, comprises an immunogenic portion of a
PT Wilms' tumor antigen.
XX
PS Disclosure; SEQ ID NO 333; 371pp; English.
XX
CC The invention relates to an isolated polypeptide comprising an
CC immunogenic portion of a Wilm's tumor antigen, or its variant that
CC differs in one or more substitutions, deletions, additions and/or
CC insertions, such that the ability of the variant to react with WT1-
CC specific antisera and/or T-cell lines or clones is not substantially
CC diminished. The composition and methods are useful in diagnosing,
CC preventing or treating malignant diseases, such as cancer or leukemia.
CC This sequence represents a protein of the invention.
XX
SQ Sequence 410 AA;

```
  Query Match             98.2%;  Score 1418.5;  DB 7;  Length 410;
  Best Local Similarity   89.2%;  Pred. No. 3.5e-102;
  Matches  256;  Conservative    0;  Mismatches    0;  Indels   31;  Gaps    1;

Qy          1 MQHHHHHH----------------------------GSDVRDLNALLPAVPSLGGGG 29
              ||||||||                            |||||||||||||||||||||
Db        124 MQHHHHHHVSIEGRASSGGSGLVPRGSSGSGDDDDKSSRGSDVRDLNALLPAVPSLGGGG 183

Qy         30 GCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPPPPPPPPPHSFIKQEPSWGGAE 89
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPPPPPPPPPHSFIKQEPSWGGAE 243

Qy         90 PHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQP 149
```

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 PHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQP 303

Qy        150 AIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYGC 209
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 AIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYGC 363

Qy        210 HTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQMNLGATLKG 256
                ||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 HTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQMNLGATLKG 410


RESULT 10
ADJ83688
ID   ADJ83688 standard; protein; 410 AA.
XX
AC   ADJ83688;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human WT1 (Wilms tumour)-related Trx_WT1_A protein.
XX
KW   immune response; WT1; Wilms tumour; immunostimulant; cytostatic; vaccine;
KW   malignant disease; leukaemia; cancer; human; Trx_WT1_A.
XX
OS   Homo sapiens.
OS   Unidentified.
XX
PN   US2003235557-A1.
XX
PD   25-DEC-2003.
XX
PF   16-SEP-2002; 2002US-00244830.
XX
PR   30-SEP-1998;   98US-00164223.
PR   25-MAR-1999;   99US-00276484.
PR   06-OCT-2000; 2000US-00684361.
PR   09-OCT-2000; 2000US-00685830.
PR   15-FEB-2001; 2001US-00785019.
PR   24-AUG-2001; 2001US-00938864.
PR   30-OCT-2001; 2001US-00002603.
PR   16-APR-2002; 2002US-00125635.
PR   12-JUL-2002; 2002US-00195835.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Gaiger A,  Cheever MA;
XX
DR   WPI; 2004-070542/07.
DR   N-PSDB; ADJ83683.
XX
PT   Inducing an immune response in an animal, useful for treating or
PT   preventing cancer, comprises administering a composition comprising a
PT   viral vector comprising an immunogenic portion of a WT1 polynucleotide.
XX
PS   Example 9; SEQ ID NO 333; 229pp; English.
XX
CC   The invention relates to a novel method for inducing an immune response
CC   in an animal which involves administering a first and a second
CC   composition comprising a first and a second viral vector, respectively,
CC   each having at least an immunogenic portion of a WT1 (Wilms tumour)
CC   polynucleotide operably linked to an expression control sequence. The
CC   method of the invention has immunostimulant and cytostatic applications
CC   and may be useful for generating or enhancing an immune response to WT1,
CC   possibly via the production of a vaccine, as well as for preventing
CC   and/or treating malignant diseases such as leukaemia and cancer. The
CC   current sequence is that of the human WT1-related protein of the
CC   invention.
XX
SQ   Sequence 410 AA;

  Query Match             98.2%;  Score 1418.5;  DB 8;  Length 410;
  Best Local Similarity   89.2%;  Pred. No. 3.5e-102;
  Matches  256;  Conservative    0;  Mismatches    0;  Indels   31;  Gaps    1;

Qy          1 MQHHHHHH----------------------------GSDVRDLNALLPAVPSLGGGG 29
                ||||||||                            ||||||||||||||||||||
Db        124 MQHHHHHHVSIEGRASSGGSGLVPRGSSGSGDDDDKSSRGSDVRDLNALLPAVPSLGGGG 183

Qy         30 GCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPPPPPPPPPHSFIKQEPSWGGAE 89
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPPPPPPPPPHSFIKQEPSWGGAE 243

Qy         90 PHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQP 149
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 PHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQP 303

Qy        150 AIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYGC 209
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 AIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYGC 363

Qy        210 HTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQMNLGATLKG 256
                ||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 HTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQMNLGATLKG 410


RESULT 11
ADL57576
ID   ADL57576 standard; protein; 410 AA.
XX
AC   ADL57576;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Human Trx-WT-1A fusion protein.
XX
KW   Human; Wilms' tumour; WT1; cancer; cytostatic; immunogen; antigen;
KW   vaccine; T-cell; MHC; Major Histocompatibility Complex; HLA-A2;
KW   human leukocyte antigen; Ra12; HIS tag; twin arginine translocator; TAT;
KW   malignant disease; fusion protein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US2003215458-A1.
XX
PD   20-NOV-2003.
XX
PF   30-OCT-2002; 2002US-00286333.
XX
PR   30-SEP-1998;   98US-00164223.
PR   25-MAR-1999;   99US-00276484.
PR   06-OCT-2000; 2000US-00684361.
PR   09-OCT-2000; 2000US-00685830.
PR   15-FEB-2001; 2001US-00785019.
PR   24-AUG-2001; 2001US-00938864.
PR   30-OCT-2001; 2001US-00002603.
PR   16-APR-2002; 2002US-00125635.
PR   12-JUL-2002; 2002US-00195835.
PR   16-SEP-2002; 2002US-00244830.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Gaiger A,  Mcneill PD,  Jaya N;
XX
DR   WPI; 2004-021827/02.
DR   N-PSDB; ADL57571.
XX
PT   New polypeptides and polynucleotides useful for generating or enhancing
PT   an immune response to Wilms' tumor, or for treating and/or preventing
PT   malignant diseases, e.g. cancer.
XX
PS   Example 9; SEQ ID NO 333; 259pp; English.
XX
CC   The invention relates to an isolated polypeptide comprising an
CC   immunogenic portion of a Wilms' tumour antigen (WT1), or their variants
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CC   that differs in substitution(s), deletion(s), addition(s) and/or
CC   insertion(s), where ability of the variant to react with WT1-specific
CC   antisera and/or T-cell lines or clones is not substantially diminished.
CC   Also included are a fusion protein comprising at least one WT1
CC   polypeptide, an isolated polynucleotide encoding the fusion protein, a
CC   composition comprising a WT1 polypeptide in combination with a
CC   pharmaceutical carrier or excipient, a vaccine comprising a WT1
CC   polypeptide in combination with a non-specific immune response enhancer,
CC   an expression vector comprising the polynucleotide operably linked to an
CC   expression control sequence and a host cell transformed or transfected
CC   with the expression vector. The immunogenic portion of the WT1
CC   polypeptide has been modified such that the ability of the immunogenic
CC   portion to bind to an MHC (Major Histocompatibility Complex) molecule or
CC   to HLA-A2 is increased relative to that of the immunogenic portion. The
CC   WT1 polypeptide may comprise a Wilms' tumour antigen having a deletion of
CC   a proline rich region at amino acid positions 54-68 of the Wilms' tumour
CC   antigen. The fusion partner is selected from Ra12, protein D, LYTA, a HIS
CC   tag, a targeting signal capable of directing a polypeptide to the
CC   endosomal/lysosomal compartment, twin arginine translocator (TAT), and
CC   truncated twin arginine translocator. The polypeptide, polynucleotide or
CC   compositions comprising them may be used for generating or enhancing an
CC   immune response to Wilms' tumour, and for treating and/or preventing
CC   malignant diseases, e.g. cancer. The compositions may be used as markers
CC   for the progression of cancer. The present sequence is a human WT-1
CC   fusion protein sequence.
XX
SQ   Sequence 410 AA;

  Query Match             98.2%;  Score 1418.5;  DB 8;  Length 410;
  Best Local Similarity   89.2%;  Pred. No. 3.5e-102;
  Matches  256;  Conservative    0;  Mismatches    0;  Indels   31;  Gaps    1;

Qy          1 MQHHHHHH------------------------------GSDVRDLNALLPAVPSLGGGG 29
              ||||||||                              ||||||||||||||||||||
Db        124 MQHHHHHHVSIEGRASSGGSGLVPRGSSGSGDDDDKSSRGSDVRDLNALLPAVPSLGGGG 183

Qy         30 GCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPPPPPPPPPHSFIKQEPSWGGAE 89
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPPPPPPPPPHSFIKQEPSWGGAE 243

Qy         90 PHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQP 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 PHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQP 303

Qy        150 AIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYGC 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 AIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYGC 363

Qy        210 HTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQMNLGATLKG 256
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 HTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQMNLGATLKG 410


RESULT 12
ADO09131
ID   ADO09131 standard; protein; 410 AA.
XX
AC   ADO09131;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human Trx_WT1_A.
XX
KW   Wilms' tumour antigen; WT1; vaccine; malignant disease; immunogenic;
KW   leukaemia; cancer; human.
XX
OS   Homo sapiens.
XX
PN   US2004018204-A1.
XX
PD   29-JAN-2004.
XX
PF   30-APR-2003; 2003US-00427717.
XX
PR   24-AUG-2001; 2001US-00938864.
PR   30-OCT-2001; 2001US-00002603.
PR   16-APR-2002; 2002US-00125635.
PR   12-JUL-2002; 2002US-00195835.
PR   16-SEP-2002; 2002US-00244830.
PR   30-OCT-2002; 2002US-00286333.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Gaiger A,  Mcneill PD,  Jaya N;
XX
DR   WPI; 2004-121992/12.
DR   N-PSDB; ADO09126.
XX
PT   New polypeptides and polynucleotides comprising an immunogenic portion of
PT   a Wilms' tumor antigen, useful as vaccines for preventing or treating
PT   malignant diseases, e.g. cancer or leukemia.
XX
PS   Example 9; SEQ ID NO 333; 252pp; English.
XX
CC   The invention relates to an isolated polypeptide which comprises an
CC   immunogenic portion of a Wilms' tumour antigen having a deletion of a
CC   proline rich region, so that the ability of the variant to react with WT1
CC   -specific antisera and/or T-cell lines or clones is not substantially
CC   diminished. The polypeptide is useful as a vaccine in combination with a
CC   non-specific immune response enhancer for preventing malignant diseases.
CC   The polypeptide is useful for enhancing or inducing an immune response in
CC   a patient; for inhibiting the development of malignant disease in a
CC   patient; for stimulating or expanding T cells. The polypeptides,
CC   polynucleotides and compositions are useful for treating malignant
CC   diseases including leukaemia and cancer. The present sequence represents
CC   the amino acid sequence of a human WT1.
XX
SQ   Sequence 410 AA;

  Query Match             98.2%;  Score 1418.5;  DB 8;  Length 410;
  Best Local Similarity   89.2%;  Pred. No. 3.5e-102;
  Matches  256;  Conservative    0;  Mismatches    0;  Indels   31;  Gaps    1;

Qy          1 MQHHHHHH------------------------------GSDVRDLNALLPAVPSLGGGG 29
              ||||||||                              ||||||||||||||||||||
Db        124 MQHHHHHHVSIEGRASSGGSGLVPRGSSGSGDDDDKSSRGSDVRDLNALLPAVPSLGGGG 183

Qy         30 GCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPPPPPPPPPHSFIKQEPSWGGAE 89
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPPPPPPPPPHSFIKQEPSWGGAE 243

Qy         90 PHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQP 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 PHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQP 303

Qy        150 AIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYGC 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 AIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYGC 363

Qy        210 HTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQMNLGATLKG 256
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 HTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQMNLGATLKG 410


RESULT 13
ABG33383
ID   ABG33383 standard; protein; 591 AA.
XX
AC   ABG33383;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Human Trx_WT1.
XX
KW   Human; mouse; cytostatic; immunostimulant; WT1; cancer; immune response.
XX
```

OS Homo sapiens.
XX
PN WO200228414-A1.
XX
PD 11-APR-2002.
XX
PF 03-OCT-2001; 2001WO-US031139.
XX
PR 06-OCT-2000; 2000US-00684361.
PR 09-OCT-2000; 2000US-00685830.
PR 15-FEB-2001; 2001US-00785019.
PR 24-AUG-2001; 2001US-00938864.
XX
PA (CORI-) CORIXA CORP.
PA (GAIG/) GAIGER A.
XX
PI Gaiger A, Mcneill PD, Smithgall M, Moulton G, Vedvick TS;
PI Sleath PR, Mossman S, Evans L, Spies AG, Boydston J;
XX
DR WPI; 2002-352217/38.
DR N-PSDB; ABK69665.
XX
PT Novel isolated WT1 polynucleotide, and encoded polypeptide, useful for
PT treating and diagnosing cancer in a patient.
XX
PS Claim 2; Page 222-223; 260pp; English.
XX
CC The invention relates to an isolated WT1 polynucleotide (I) and
CC polypeptide encoded by (I). The WT1 polynucleotides and polypeptides are
CC used for treating and detecting cancer in a patient, and for stimulating
CC an immune response in patient. ABG33070-ABG33405 represent WT1 amino acid
CC sequences of the invention
XX
SQ Sequence 591 AA;

Query Match 98.2%; Score 1418; DB 5; Length 591;
Best Local Similarity 88.9%; Pred. No. 5.8e-102;
Matches 256; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

```
Qy          1 MQHHHHHH----------------------------------GSDVRDLNALLPAVPSLGGG 28
              ||||||||                                  ||||||||||||||||||||
Db        124 MQHHHHHHVSIEGRASSGGSGLVPRGSSGSGDDDDKSSRMGSDVRDLNALLPAVPSLGGG 183

Qy         29 GGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPPPPPPPPPHSFIKQEPSWGGA 88
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPPPPPPPPPHSFIKQEPSWGGA 243

Qy         89 EPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQ 148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 EPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQ 303

Qy        149 PAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYG 208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 PAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYG 363

Qy        209 CHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQMNLGATLKG 256
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 CHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQMNLGATLKG 411
```

RESULT 14
ADB67536
ID ADB67536 standard; protein; 591 AA.
XX
AC ADB67536;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human WT1-Trx fusion protein.
XX
KW Human; Wilm's tumour antigen; WT1; cytostatic; antigen; T cell;
KW antigen-presenting cell; CD4+; CD8+; immune response; cancer; vaccine;
KW leukaemia; antigen.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US2003072767-A1.
XX
PD 17-APR-2003.
XX
PF 24-AUG-2001; 2001US-00938864.
XX
PR 30-SEP-1998; 98US-00164223.
PR 25-MAR-1999; 99US-00276484.
PR 06-OCT-2000; 2000US-00684361.
PR 09-OCT-2000; 2000US-00685830.
PR 15-FEB-2001; 2001US-00785019.
XX
PA (GAIG/) GAIGER A.
PA (MCNE/) MCNEILL P D.
PA (SMIT/) SMITHGALL M.
PA (MOUL/) MOULTON G.
PA (VEDV/) VEDVICK T S.
PA (SLEA/) SLEATH P R.
PA (MOSS/) MOSSMAN S.
PA (EVAN/) EVANS L.
PA (SPIE/) SPIES A G.
PA (BOYD/) BOYDSTON J.
XX
PI Gaiger A, Mcneill PD, Smithgall M, Moulton G, Vedvick TS;
PI Sleath PR, Mossman S, Evans L, Spies AG, Boydston J;
XX
DR WPI; 2003-605957/57.
DR N-PSDB; ADB67531.
XX
PT Novel Wilms tumor polynucleotides encoding WT1 polypeptides, useful for
PT detecting the presence of cancer in a patient, and in pharmaceutical
PT compositions, e.g. vaccines, for treating cancers e.g. leukemia.
XX
PS Claim 2; Page 125-127; 197pp; English.
XX
CC The invention relates to an isolated Wilm tumour (WT1) polynucleotide
CC comprising a full length protein, truncated protein, mutated protein or
CC fusion protein. Also included are the encoded WT1 proteins, expression
CC vectors, host cells, antibodies, detecting the presence of a cancer in a
CC patient by contacting a biological sample with a binding agent that binds
CC to a WT1 protein, an oligonucleotide that hybridises to a WT1
CC polynucleotide, stimulating and/or expanding T cells specific for a
CC tumour protein by contacting T cells with the WT1 polynucleotide, the WT1
CC protein or antigen-presenting cells that express the WT1 protein, a
CC composition (C1) (comprising physiologically acceptable carriers and
CC immunostimulants as first component, and a second component selected from
CC the WT1 polynucleotide, the WT1 protein, Ab, or T cells and antigen
CC presenting cells that express the WT1 protein), inhibiting the
CC development of a cancer in a patient (by incubating CD4+ and/or CD8+ T
CC cells isolated from a patient with the WT1 polynucleotide, the WT1
CC protein or antigen presenting cells that express the WT1 protein, such
CC that T cell proliferate, administering the proliferated T cells to the
CC patient, and thus inhibiting the development of a cancer in the patient)
CC and a composition (C2) (comprising a WT1 polypeptide resuspended in a
CC buffer comprising at least 1-3 sugars selected from trehalose, maltose,
CC sucrose, fructose and glucose, at a concentration of 7-13%, and
CC optionally ethanolamine, cysteine and Polysorbate-80, or WT1 polypeptide
CC and MPL-SE or Enhanzyn). Also disclosed as anew are polypeptides
CC comprising a variant of an immunogenic portion of WT1 polypeptide. C1 is
CC useful for stimulating immune response in a patient, and for treating
CC cancer in a patient. The oligonucleotide is also useful for determining
CC the presence of a cancer in a patient. The WT1 polynucleotide and the WT1
CC protein are useful in pharmaceutical compositions, e.g. vaccines. the WT1
CC protein is useful as marker to indicate the presence or absence of a
CC cancer. C1 is useful for inhibiting the development of a malignant
CC disease in a patient, for preventing and treating metastatic diseases
CC e.g. leukaemia and cancer, and for removing tumour cells from a
CC biological sample. Ab (binding agent for the WT1 protein) is useful for
CC detecting the presence of cancer in a patient. The present sequence

```
CC   represents a Human WT1 fusion protein.
XX
SQ   Sequence 591 AA;

  Query Match             98.2%;  Score 1418;  DB 7;  Length 591;
  Best Local Similarity   88.9%;  Pred. No. 5.8e-102;
  Matches  256;  Conservative    0;  Mismatches    0;  Indels   32;  Gaps    1;

Qy          1 MQHHHHHH--------------------------------GSDVRDLNALLPAVPSLGGG 28
              ||||||||                                ||||||||||||||||||||
Db        124 MQHHHHHHVSIEGRASSGGSGLVPRGSSGSGDDDDKSSRMGSDVRDLNALLPAVPSLGGG 183

Qy         29 GGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPPPPPPPPPHSFIKQEPSWGGA 88
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Db        184 GGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPPPPPPPPPHSFIKQEPSWGGA 243

Qy         89 EPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQ 148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 EPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQ 303

Qy        149 PAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYG 208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 PAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYG 363

Qy        209 CHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQMNLGATLKG 256
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 CHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQMNLGATLKG 411


RESULT 15
ADJ80769
ID   ADJ80769 standard; protein; 591 AA.
XX
AC   ADJ80769;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Wilm's tumor antigen associated protein #3.
XX
KW   cytostatic; gene therapy; vaccine; Wilm's tumor antigen; WT1; cancer;
KW   leukemia.
XX
OS   Homo sapiens.
XX
PN   WO2003037060-A2.
XX
PD   08-MAY-2003.
XX
PF   30-OCT-2002; 2002WO-US035194.
XX
PR   30-OCT-2001; 2001US-00002603.
PR   16-APR-2002; 2002US-00125635.
PR   12-JUL-2002; 2002US-00195835.
PR   16-SEP-2002; 2002US-00244830.
XX
PA   (CORI-) CORIXA CORP.
PA   (GAIG/) GAIGER A.
XX
PI   Gaiger A,  Mcneill PD,  Jaya N,  Carter D;
XX
DR   WPI; 2003-430453/40.
XX
PT   New isolated polypeptide for diagnosing, preventing or treating malignant
PT   diseases, e.g. cancer or leukemia, comprises an immunogenic portion of a
PT   Wilms' tumor antigen.
XX
PS   Disclosure; SEQ ID NO 334; 371pp; English.
XX
CC   The invention relates to an isolated polypeptide comprising an
CC   immunogenic portion of a Wilm's tumor antigen, or its variant that
CC   differs in one or more substitutions, deletions, additions and/or
CC   insertions, such that the ability of the variant to react with WT1-
CC   specific antisera and/or T-cell lines or clones is not substantially
CC   diminished. The composition and methods are useful in diagnosing,
CC   preventing or treating malignant diseases, such as cancer or leukemia.
CC   This sequence represents a protein of the invention.
XX
SQ   Sequence 591 AA;

  Query Match             98.2%;  Score 1418;  DB 7;  Length 591;
  Best Local Similarity   88.9%;  Pred. No. 5.8e-102;
  Matches  256;  Conservative    0;  Mismatches    0;  Indels   32;  Gaps    1;

Qy          1 MQHHHHHH--------------------------------GSDVRDLNALLPAVPSLGGG 28
              ||||||||                                ||||||||||||||||||||
Db        124 MQHHHHHHVSIEGRASSGGSGLVPRGSSGSGDDDDKSSRMGSDVRDLNALLPAVPSLGGG 183

Qy         29 GGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPPPPPPPPPHSFIKQEPSWGGA 88
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPPPPPPPPPHSFIKQEPSWGGA 243

Qy         89 EPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQ 148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 EPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQ 303

Qy        149 PAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYG 208
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 PAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYG 363

Qy        209 CHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQMNLGATLKG 256
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 CHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQMNLGATLKG 411


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Job time : 168 secs
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OM protein - protein search, using sw model

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Perfect score: 1444
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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1386	96.0	429	1	US-08-234-783-4	Sequence 4, Appli
2	1386	96.0	429	1	US-08-456-907-4	Sequence 4, Appli
3	1386	96.0	429	5	PCT-US95-05523-4	Sequence 4, Appli
4	1386	96.0	449	1	US-08-102-942A-6	Sequence 6, Appli
5	1386	96.0	449	3	US-09-037-179B-6	Sequence 6, Appli
6	1386	96.0	449	4	US-09-538-092-960	Sequence 960, App
7	1386	96.0	559	4	US-09-949-016-9138	Sequence 9138, Ap
8	1386	96.0	559	4	US-09-949-016-9139	Sequence 9139, Ap
9	1386	96.0	559	4	US-09-949-016-9140	Sequence 9140, Ap
10	1386	96.0	559	4	US-09-949-016-9141	Sequence 9141, Ap
11	1386	96.0	576	4	US-09-949-016-9404	Sequence 9404, Ap
12	1386	96.0	576	4	US-09-949-016-9405	Sequence 9405, Ap
13	1386	96.0	576	4	US-09-949-016-9406	Sequence 9406, Ap
14	1386	96.0	576	4	US-09-949-016-9407	Sequence 9407, Ap
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16	1329	92.0	449	3	US-09-037-179B-4	Sequence 4, Appli
17	1051	72.8	210	1	US-08-234-783-2	Sequence 2, Appli
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20	917	63.5	345	1	US-08-102-942A-2	Sequence 2, Appli
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22	849	58.8	154	1	US-08-102-942A-5	Sequence 5, Appli
23	849	58.8	154	3	US-09-037-179B-5	Sequence 5, Appli
24	140	9.7	503	4	US-09-949-016-9746	Sequence 9746, Ap
25	139	9.6	1274	3	US-09-095-443-2	Sequence 2, Appli
26	138.5	9.6	971	4	US-09-538-092-1332	Sequence 1332, Ap
27	135.5	9.4	945	4	US-09-248-796A-15743	Sequence 15743, A
28	135.5	9.4	1007	4	US-10-144-198-36	Sequence 36, Appl
29	135.5	9.4	1041	4	US-10-144-198-14	Sequence 14, Appl
30	135	9.3	707	4	US-09-919-039-278	Sequence 278, App
31	135	9.3	707	4	US-09-538-092-993	Sequence 993, App
32	135	9.3	735	4	US-09-949-016-10120	Sequence 10120, A
33	135	9.3	1315	3	US-08-899-595-3	Sequence 3, Appli
34	134	9.3	780	4	US-09-949-016-10205	Sequence 10205, A
35	134	9.3	1184	4	US-09-266-225D-18	Sequence 18, Appl
36	133	9.2	684	4	US-09-823-240A-9	Sequence 9, Appli
37	133	9.2	1248	2	US-09-080-897-2	Sequence 2, Appli
38	133	9.2	1248	3	US-09-323-735-2	Sequence 2, Appli
39	129.5	9.0	693	4	US-09-949-016-7806	Sequence 7806, Ap
40	129.5	9.0	1185	3	US-09-041-886-23	Sequence 23, Appl
41	129.5	9.0	1185	4	US-09-538-092-1209	Sequence 1209, Ap
42	129	8.9	345	1	US-08-031-148-4	Sequence 4, Appli
43	129	8.9	345	3	US-08-415-838-4	Sequence 4, Appli
44	129	8.9	345	3	US-09-205-169-4	Sequence 4, Appli
45	129	8.9	697	4	US-09-949-016-9660	Sequence 9660, Ap

ALIGNMENTS

```
RESULT 1
US-08-234-783-4
; Sequence 4, Application US/08234783
; Patent No. 5622835
;  GENERAL INFORMATION:
;    APPLICANT:  Herlyn, Meenhard
;    APPLICANT:  Morris, Jennifer
;    APPLICANT:  Rauscher III, Frank J.
;    APPLICANT:  Rodeck, Ulrich
;    TITLE OF INVENTION:  WT1 Monoclonal Antibodies and Methods of
;    TITLE OF INVENTION:  Use Therefor
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Cntr, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/234,783
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST48USA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9200
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  429 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-234-783-4

  Query Match             96.0%;  Score 1386;  DB 1;  Length 429;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-110;
  Matches  248;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 61
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Qy          69 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 128
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Db          62 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 121

Qy         129 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 188
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         122 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 181

Qy         189 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 248
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         182 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 241

Qy         249 NLGATLKG 256
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Db         242 NLGATLKG 249


RESULT 2
US-08-456-907-4
; Sequence 4, Application US/08456907
; Patent No. 5633142
;  GENERAL INFORMATION:
;    APPLICANT:  Herlyn, Meenhard
;    APPLICANT:  Morris, Jennifer
;    APPLICANT:  Rauscher III, Frank J.
;    APPLICANT:  Rodeck, Ulrich
;    TITLE OF INVENTION:  WT1 Monoclonal Antibodies and Methods of
;    TITLE OF INVENTION:  Use Therefor
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Cntr, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/456,907
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/234,783
;      FILING DATE:  28-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST48AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9200
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  429 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-456-907-4

  Query Match             96.0%;  Score 1386;  DB 1;  Length 429;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-110;
  Matches  248;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           9 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 68
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           2 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 61

Qy          69 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 128
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          62 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 121

Qy         129 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 188
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         122 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 181

Qy         189 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 248
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         182 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 241

Qy         249 NLGATLKG 256
               ||||||||
Db         242 NLGATLKG 249


RESULT 3
PCT-US95-05523-4
; Sequence 4, Application PC/TUS9505523
;  GENERAL INFORMATION:
;    APPLICANT:  The Wistar Institute of Anatomy and Biology
;    TITLE OF INVENTION:  WT1 Monoclonal Antibodies and
;    TITLE OF INVENTION:  Methods of Use Therefor
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Cntr, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/05523
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/234,783
;      FILING DATE:  28-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST48PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9200
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  429 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-05523-4

  Query Match             96.0%;  Score 1386;  DB 5;  Length 429;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-110;
  Matches  248;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           9 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 68
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           2 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 61

Qy          69 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 128
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          62 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 121

Qy         129 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 188
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         122 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 181
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Qy        189 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 241

Qy        249 NLGATLKG 256
              ||||||||
Db        242 NLGATLKG 249


RESULT 4
US-08-102-942A-6
; Sequence 6, Application US/08102942A
; Patent No. 5726288
;  GENERAL INFORMATION:
;    APPLICANT:  Call, Katherine M.
;    APPLICANT:  Glaser, Thomas M.
;    APPLICANT:  Ito, Caryn Y.
;    APPLICANT:  Buckler, Alan J.
;    APPLICANT:  Pelletier, Jerry
;    APPLICANT:  Haber, Daniel A.
;    APPLICANT:  Rose, Elise A.
;    APPLICANT:  Housman, David E.
;    APPLICANT:  Bruening, Wendy
;    APPLICANT:  Darveau, Andre
;    TITLE OF INVENTION:  Localization and Characterization of the
;    TITLE OF INVENTION:  Wilms' Tumor Gene
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  U.S.
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/102,942A
;      FILING DATE:  02-AUG-1993
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  MIT-5194A2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-861-6240
;      TELEFAX:  617-861-9540
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  449 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-102-942A-6

  Query Match             96.0%;  Score 1386;  DB 1;  Length 449;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-110;
  Matches  248;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 61

Qy         69 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 121

Qy        129 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 181

Qy        189 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 241

Qy        249 NLGATLKG 256
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Db        242 NLGATLKG 249


RESULT 5
US-09-037-179B-6
; Sequence 6, Application US/09037179B
; Patent No. 6316599
; GENERAL INFORMATION:
;  APPLICANT: Call, Katherine M.
;  APPLICANT:  Glaser, Thomas M.
;  APPLICANT:  Ito, Caryn Y.
;  APPLICANT:  Buckler, Alan J.
;  APPLICANT:  Pelletier, Jerry
;  APPLICANT:  Haber, Daniel A.
;  APPLICANT:  Rose, Elise A.
;  APPLICANT:  Housman, David E.
;  APPLICANT:  Bruening, Wendy
;  APPLICANT:  Darveau, Andre
;  TITLE OF INVENTION: Localization and Characterization of the
;  TITLE OF INVENTION:  Wilms' Tumor Gene
;  FILE REFERENCE: 0050.1312-011
;  CURRENT APPLICATION NUMBER: US/09/037,179B
;  CURRENT FILING DATE:  1998-03-09
;  PRIOR APPLICATION NUMBER: US 08/102,942
;  PRIOR FILING DATE: 1993-08-02
;  PRIOR APPLICATION NUMBER: US 07/614,161
;  PRIOR FILING DATE: 1990-11-13
;  PRIOR APPLICATION NUMBER: US 07/435,780
;  PRIOR FILING DATE: 1989-11-13
;  PRIOR APPLICATION NUMBER: US 07/795,323
;  PRIOR FILING DATE: 1994-09-27
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 449
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-037-179B-6

  Query Match             96.0%;  Score 1386;  DB 3;  Length 449;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-110;
  Matches  248;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 68
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Db          2 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 61

Qy         69 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 121

Qy        129 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 188
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Db        122 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 181

Qy        189 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 241

Qy        249 NLGATLKG 256
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Db        242 NLGATLKG 249
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RESULT 6
US-09-538-092-960
; Sequence 960, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
;  APPLICANT: Giot, Loic
;  APPLICANT:  Mansfield, Traci A.
;  TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
;  FILE REFERENCE: 15966-542
;  CURRENT APPLICATION NUMBER: US/09/538,092
;  CURRENT FILING DATE:  2000-03-29
;  PRIOR APPLICATION NUMBER: 60/127,352
;  PRIOR FILING DATE: 1999-04-01
;  PRIOR APPLICATION NUMBER: 60/178,965
;  PRIOR FILING DATE: 2000-02-01
;  NUMBER OF SEQ ID NOS: 1387
;  SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 960
;   LENGTH: 449
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Polypeptide Accession Number P19544
US-09-538-092-960

  Query Match             96.0%;  Score 1386;  DB 4;  Length 449;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-110;
  Matches  248;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 61

Qy         69 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 128
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Db         62 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 121

Qy        129 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 181

Qy        189 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 241

Qy        249 NLGATLKG 256
              ||||||||
Db        242 NLGATLKG 249


RESULT 7
US-09-949-016-9138
; Sequence 9138, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9138
;   LENGTH: 559
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-9138

  Query Match             96.0%;  Score 1386;  DB 4;  Length 559;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-110;
  Matches  248;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 191

Qy         69 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 251

Qy        129 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 311

Qy        189 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 371

Qy        249 NLGATLKG 256
              ||||||||
Db        372 NLGATLKG 379


RESULT 8
US-09-949-016-9139
; Sequence 9139, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9139
;   LENGTH: 559
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-9139

  Query Match             96.0%;  Score 1386;  DB 4;  Length 559;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-110;
  Matches  248;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 191

Qy         69 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 251

Qy        129 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 311

Qy        189 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 371
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Qy        249 NLGATLKG 256
              ||||||||
Db        372 NLGATLKG 379


RESULT 9
US-09-949-016-9140
; Sequence 9140, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9140
;   LENGTH: 559
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-9140

  Query Match             96.0%;  Score 1386;  DB 4;  Length 559;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-110;
  Matches  248;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 191

Qy         69 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 251

Qy        129 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 311

Qy        189 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 248
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Db        312 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 371

Qy        249 NLGATLKG 256
              ||||||||
Db        372 NLGATLKG 379


RESULT 10
US-09-949-016-9141
; Sequence 9141, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9141
;   LENGTH: 559
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-9141

  Query Match             96.0%;  Score 1386;  DB 4;  Length 559;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-110;
  Matches  248;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 191

Qy         69 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 251

Qy        129 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 311

Qy        189 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 371

Qy        249 NLGATLKG 256
              ||||||||
Db        372 NLGATLKG 379


RESULT 11
US-09-949-016-9404
; Sequence 9404, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9404
;   LENGTH: 576
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-9404

  Query Match             96.0%;  Score 1386;  DB 4;  Length 576;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-110;
  Matches  248;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 191

Qy         69 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 251

Qy        129 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 311
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Qy        189 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 371

Qy        249 NLGATLKG 256
              ||||||||
Db        372 NLGATLKG 379


RESULT 12
US-09-949-016-9405
; Sequence 9405, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9405
;   LENGTH: 576
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-9405

  Query Match             96.0%;  Score 1386;  DB 4;  Length 576;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-110;
  Matches  248;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 191

Qy         69 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 251

Qy        129 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 311

Qy        189 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 371

Qy        249 NLGATLKG 256
              ||||||||
Db        372 NLGATLKG 379


RESULT 13
US-09-949-016-9406
; Sequence 9406, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9406
;   LENGTH: 576
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-9406

  Query Match             96.0%;  Score 1386;  DB 4;  Length 576;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-110;
  Matches  248;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 191

Qy         69 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 251

Qy        129 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 188
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Qy        189 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 248
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Qy        249 NLGATLKG 256
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Db        372 NLGATLKG 379


RESULT 14
US-09-949-016-9407
; Sequence 9407, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9407
;   LENGTH: 576
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-9407

  Query Match             96.0%;  Score 1386;  DB 4;  Length 576;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-110;
  Matches  248;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 191

Qy         69 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 128
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Qy        129 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 188
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Qy        249 NLGATLKG 256
              ||||||||
Db        372 NLGATLKG 379
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RESULT 15
US-08-102-942A-4
; Sequence 4, Application US/08102942A
; Patent No. 5726288
; GENERAL INFORMATION:
; APPLICANT: Call, Katherine M.
; APPLICANT: Glaser, Thomas M.
; APPLICANT: Ito, Caryn Y.
; APPLICANT: Buckler, Alan J.
; APPLICANT: Pelletier, Jerry
; APPLICANT: Haber, Daniel A.
; APPLICANT: Rose, Elise A.
; APPLICANT: Housman, David E.
; APPLICANT: Bruening, Wendy
; APPLICANT: Darveau, Andre
; TITLE OF INVENTION: Localization and Characterization of the
; TITLE OF INVENTION: Wilms' Tumor Gene
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/102,942A
; FILING DATE: 02-AUG-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-5194A2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-102-942A-4

Query Match 92.0%; Score 1329; DB 1; Length 449;
Best Local Similarity 96.8%; Pred. No. 1e-105;
Matches 241; Conservative 1; Mismatches 5; Indels 2; Gaps 2;

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Db          2 GSDVRDLNALLPAVSSLGGGGGGGCGLPVSGARQWAPVLDFAPPGASAYGSLGGPAPPPA- 60

Qy         68 PPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQA 127
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Qy        128 SSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHED 187
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Qy        188 PMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQ 247
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Qy        248 MNLGATLKG 256
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Db        241 MNLGATLKG 249
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OM protein - protein search, using sw model

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(without alignments)
632.602 Million cell updates/sec

Title: US-09-785-019B-335
Perfect score: 1444
Sequence: 1 MQHHHHHHGSDVRDLNALLP.....TSQLECMTWNQMNLGATLKG 256

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Gapop 10.0 , Gapext 0.5

Searched: 1428581 seqs, 333598853 residues

Total number of hits satisfying chosen parameters: 1428581

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1444	100.0	256	10	US-09-785-019-335	Sequence 335, App
3	1444	100.0	256	14	US-10-125-635A-335	Sequence 335, App
4	1444	100.0	256	14	US-10-002-603-335	Sequence 335, App
5	1444	100.0	256	14	US-10-195-835-335	Sequence 335, App
6	1444	100.0	256	15	US-10-286-333-335	Sequence 335, App
7	1444	100.0	256	15	US-10-244-830-335	Sequence 335, App
8	1444	100.0	256	15	US-10-427-717-335	Sequence 335, App
9	1444	100.0	256	16	US-10-648-780-335	Sequence 335, App
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11	1418.5	98.2	410	10	US-09-785-019-333	Sequence 333, App
12	1418.5	98.2	410	14	US-10-125-635A-333	Sequence 333, App
13	1418.5	98.2	410	14	US-10-002-603-333	Sequence 333, App
14	1418.5	98.2	410	14	US-10-195-835-333	Sequence 333, App
15	1418.5	98.2	410	15	US-10-286-333-333	Sequence 333, App
16	1418.5	98.2	410	15	US-10-244-830-333	Sequence 333, App
17	1418.5	98.2	410	15	US-10-427-717-333	Sequence 333, App
18	1418.5	98.2	410	16	US-10-648-780-333	Sequence 333, App
19	1418	98.2	591	10	US-09-938-864-334	Sequence 334, App
20	1418	98.2	591	10	US-09-785-019-334	Sequence 334, App
21	1418	98.2	591	14	US-10-125-635A-334	Sequence 334, App
22	1418	98.2	591	14	US-10-002-603-334	Sequence 334, App
23	1418	98.2	591	14	US-10-195-835-334	Sequence 334, App
24	1418	98.2	591	15	US-10-286-333-334	Sequence 334, App
25	1418	98.2	591	15	US-10-244-830-334	Sequence 334, App
26	1418	98.2	591	15	US-10-427-717-334	Sequence 334, App
27	1418	98.2	591	16	US-10-648-780-334	Sequence 334, App
28	1394	96.5	292	15	US-10-286-333-470	Sequence 470, App
29	1394	96.5	292	15	US-10-286-333-499	Sequence 499, App
30	1394	96.5	292	15	US-10-427-717-470	Sequence 470, App
31	1394	96.5	292	15	US-10-427-717-499	Sequence 499, App
32	1394	96.5	321	14	US-10-125-635A-455	Sequence 455, App
33	1394	96.5	321	14	US-10-195-835-455	Sequence 455, App
34	1394	96.5	321	15	US-10-286-333-455	Sequence 455, App
35	1394	96.5	321	15	US-10-286-333-479	Sequence 479, App
36	1394	96.5	321	15	US-10-244-830-455	Sequence 455, App
37	1394	96.5	321	15	US-10-427-717-455	Sequence 455, App
38	1394	96.5	321	15	US-10-427-717-479	Sequence 479, App
39	1394	96.5	321	16	US-10-648-780-455	Sequence 455, App
40	1394	96.5	469	14	US-10-125-635A-454	Sequence 454, App
41	1394	96.5	469	14	US-10-195-835-454	Sequence 454, App
42	1394	96.5	469	15	US-10-286-333-454	Sequence 454, App
43	1394	96.5	469	15	US-10-244-830-454	Sequence 454, App
44	1394	96.5	469	15	US-10-427-717-454	Sequence 454, App
45	1394	96.5	469	16	US-10-648-780-454	Sequence 454, App

ALIGNMENTS

RESULT 1
US-09-938-864-335
; Sequence 335, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-938-864-335

Query Match 100.0%; Score 1444; DB 10; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.8e-90;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MQHHHHHHGSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MQHHHHHHGSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGG 60
```

```
Qy          61 PAPPPAPPPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFG 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 PAPPPAPPPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFG 120

Qy         121 PPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPN 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 PPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPN 180

Qy         181 HSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQL 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 HSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQL 240

Qy         241 ECMTWNQMNLGATLKG 256
               ||||||||||||||||
Db         241 ECMTWNQMNLGATLKG 256
```

RESULT 2
US-09-785-019-335
; Sequence 335, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C4
; CURRENT APPLICATION NUMBER: US/09/785,019
; CURRENT FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-785-019-335

Query Match 100.0%; Score 1444; DB 10; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.8e-90;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy           1 MQHHHHHHGSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGG 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MQHHHHHHGSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGG 60

Qy          61 PAPPPAPPPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFG 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 PAPPPAPPPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFG 120

Qy         121 PPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPN 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 PPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPN 180

Qy         181 HSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQL 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 HSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQL 240

Qy         241 ECMTWNQMNLGATLKG 256
               ||||||||||||||||
Db         241 ECMTWNQMNLGATLKG 256
```

RESULT 3
US-10-125-635A-335
; Sequence 335, Application US/10125635A
; Publication No. US20030039635A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Smithgall, Molly D.
; APPLICANT: Carter, Darrick
; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C7
; CURRENT APPLICATION NUMBER: US/10/125,635A
; CURRENT FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-635A-335

Query Match 100.0%; Score 1444; DB 14; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.8e-90;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy           1 MQHHHHHHGSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGG 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MQHHHHHHGSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGG 60

Qy          61 PAPPPAPPPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFG 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 PAPPPAPPPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFG 120

Qy         121 PPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPN 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 PPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPN 180

Qy         181 HSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQL 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 HSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQL 240

Qy         241 ECMTWNQMNLGATLKG 256
               ||||||||||||||||
Db         241 ECMTWNQMNLGATLKG 256
```

RESULT 4
US-10-002-603-335
; Sequence 335, Application US/10002603
; Publication No. US20030095971A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Mossman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydston, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C6
; CURRENT APPLICATION NUMBER: US/10/002,603
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-002-603-335

Query Match 100.0%; Score 1444; DB 14; Length 256;
Best Local Similarity 100.0%; Pred. No. 1.8e-90;

```
  Matches  256;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MQHHHHHHGSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MQHHHHHHGSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGG 60

Qy         61 PAPPPAPPPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PAPPPAPPPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFG 120

Qy        121 PPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPN 180

Qy        181 HSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQL 240

Qy        241 ECMTWNQMNLGATLKG 256
              ||||||||||||||||
Db        241 ECMTWNQMNLGATLKG 256


RESULT 5
US-10-195-835-335
; Sequence 335, Application US/10195835
; Publication No. US20030198622A1
; GENERAL INFORMATION:
;  APPLICANT: Gaiger, Alexander
;  APPLICANT:  Smithgall, Molly D.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Cheever, Martin A.
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Sutherland, R. Alec
;  APPLICANT:  Mossman, Sally P.
;  APPLICANT:  Evans, Lawrence S.
;  APPLICANT:  Swanson, Ryan M.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
;  TITLE OF INVENTION:  SPECIFIC IMMUNOTHERAPY
;  FILE REFERENCE: 210121.465C8
;  CURRENT APPLICATION NUMBER: US/10/195,835
;  CURRENT FILING DATE:  2002-07-12
;  NUMBER OF SEQ ID NOS: 461
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 335
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-195-835-335

  Query Match           100.0%;  Score 1444;  DB 14;  Length 256;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-90;
  Matches  256;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MQHHHHHHGSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MQHHHHHHGSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGG 60

Qy         61 PAPPPAPPPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PAPPPAPPPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFG 120

Qy        121 PPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPN 180

Qy        181 HSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQL 240

Qy        241 ECMTWNQMNLGATLKG 256
              ||||||||||||||||
Db        241 ECMTWNQMNLGATLKG 256


RESULT 6
US-10-286-333-335
; Sequence 335, Application US/10286333
; Publication No. US20030215458A1
; GENERAL INFORMATION:
;  APPLICANT: Gaiger, Alexander
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Jaya, No. US20030215458A1alie
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
;  TITLE OF INVENTION:  SPECIFIC IMMUNOTHERAPY
;  FILE REFERENCE: 210121.465C10
;  CURRENT APPLICATION NUMBER: US/10/286,333
;  CURRENT FILING DATE:  2002-10-30
;  NUMBER OF SEQ ID NOS: 506
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 335
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-286-333-335

  Query Match           100.0%;  Score 1444;  DB 15;  Length 256;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-90;
  Matches  256;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MQHHHHHHGSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MQHHHHHHGSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGG 60

Qy         61 PAPPPAPPPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PAPPPAPPPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFG 120

Qy        121 PPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPN 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPN 180

Qy        181 HSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQL 240

Qy        241 ECMTWNQMNLGATLKG 256
              ||||||||||||||||
Db        241 ECMTWNQMNLGATLKG 256


RESULT 7
US-10-244-830-335
; Sequence 335, Application US/10244830
; Publication No. US20030235557A1
; GENERAL INFORMATION:
;  APPLICANT: Gaiger, Alexander
;  APPLICANT:  Cheever, Martin A.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
;  TITLE OF INVENTION:  SPECIFIC IMMUNOTHERAPY
;  FILE REFERENCE: 210121.465C9
;  CURRENT APPLICATION NUMBER: US/10/244,830
;  CURRENT FILING DATE:  2002-09-16
;  NUMBER OF SEQ ID NOS: 468
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 335
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-244-830-335

  Query Match           100.0%;  Score 1444;  DB 15;  Length 256;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-90;
  Matches  256;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MQHHHHHHGSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGG 60
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MQHHHHHHGSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGG 60

Qy         61 PAPPPAPPPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFG 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PAPPPAPPPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFG 120

Qy        121 PPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPN 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPN 180

Qy        181 HSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQL 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQL 240

Qy        241 ECMTWNQMNLGATLKG 256
                ||||||||||||||||
Db        241 ECMTWNQMNLGATLKG 256


RESULT 8
US-10-427-717-335
; Sequence 335, Application US/10427717
; Publication No. US20040018204A1
; GENERAL INFORMATION:
;  APPLICANT: Gaiger, Alexander
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Jaya, No. US20040018204A1alie
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
;  TITLE OF INVENTION:  SPECIFIC IMMUNOTHERAPY
;  FILE REFERENCE: 210121.465C11
;  CURRENT APPLICATION NUMBER: US/10/427,717
;  CURRENT FILING DATE:  2003-04-30
;  NUMBER OF SEQ ID NOS: 508
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 335
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-427-717-335

  Query Match             100.0%;  Score 1444;  DB 15;  Length 256;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-90;
  Matches  256;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MQHHHHHHGSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGG 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MQHHHHHHGSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGG 60

Qy         61 PAPPPAPPPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFG 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PAPPPAPPPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFG 120

Qy        121 PPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPN 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPN 180

Qy        181 HSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQL 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQL 240

Qy        241 ECMTWNQMNLGATLKG 256
                ||||||||||||||||
Db        241 ECMTWNQMNLGATLKG 256


RESULT 9
US-10-648-780-335
; Sequence 335, Application US/10648780
; Publication No. US20040126362A1
; GENERAL INFORMATION:
;  APPLICANT: Gaiger, Alexander
;  APPLICANT:  Smithgall, Molly D.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Cheever, Martin A.
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Sutherland, R. Alec
;  APPLICANT:  Mossman, Sally P.
;  APPLICANT:  Evans, Lawrence S.
;  APPLICANT:  Swanson, Ryan M.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
;  TITLE OF INVENTION:  SPECIFIC IMMUNOTHERAPY
;  FILE REFERENCE: 210121.465C8
;  CURRENT APPLICATION NUMBER: US/10/648,780
;  CURRENT FILING DATE:  2003-08-26
;  NUMBER OF SEQ ID NOS: 461
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 335
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-648-780-335

  Query Match             100.0%;  Score 1444;  DB 16;  Length 256;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-90;
  Matches  256;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MQHHHHHHGSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGG 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MQHHHHHHGSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGG 60

Qy         61 PAPPPAPPPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFG 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PAPPPAPPPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFG 120

Qy        121 PPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPN 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 PPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPN 180

Qy        181 HSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQL 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 HSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQL 240

Qy        241 ECMTWNQMNLGATLKG 256
                ||||||||||||||||
Db        241 ECMTWNQMNLGATLKG 256


RESULT 10
US-09-938-864-333
; Sequence 333, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
;  APPLICANT: Gaiger, Alexander
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Smithgall, Molly
;  APPLICANT:  Moulton, Gus
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Sleath, Paul R.
;  APPLICANT:  Mossman, Sally
;  APPLICANT:  Evans, Lawrence
;  APPLICANT:  Spies, A. Gregory
;  APPLICANT:  Boydston, Jeremy
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
;  TITLE OF INVENTION:  SPECIFIC IMMUNOTHERAPY
;  FILE REFERENCE: 210121.465C5
;  CURRENT APPLICATION NUMBER: US/09/938,864
;  CURRENT FILING DATE:  2001-08-24
;  NUMBER OF SEQ ID NOS: 413
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 333
;   LENGTH: 410
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-938-864-333
```

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  Query Match            98.2%;  Score 1418.5;  DB 10;  Length 410;
  Best Local Similarity  89.2%;  Pred. No. 1.5e-88;
  Matches  256;  Conservative    0;  Mismatches    0;  Indels   31;  Gaps    1;

Qy          1 MQHHHHHH------------------------------GSDVRDLNALLPAVPSLGGGG 29
              ||||||||                              ||||||||||||||||||||||
Db        124 MQHHHHHHVSIEGRASSGGSGLVPRGSSGSGDDDDKSSRGSDVRDLNALLPAVPSLGGGG 183

Qy         30 GCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPPPPPPPPPHSFIKQEPSWGGAE 89
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPPPPPPPPPHSFIKQEPSWGGAE 243

Qy         90 PHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQP 149
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 PHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQP 303

Qy        150 AIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYGC 209
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 AIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYGC 363

Qy        210 HTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQMNLGATLKG 256
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 HTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQMNLGATLKG 410


RESULT 11
US-09-785-019-333
; Sequence 333, Application US/09785019
; Publication No. US20030082196A1
; GENERAL INFORMATION:
;  APPLICANT: Gaiger, Alexander
;  APPLICANT:  Cheever, Martin A.
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Smithgall, Molly
;  APPLICANT:  Moulton, Gus
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Sleath, Paul
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
;  TITLE OF INVENTION:  SPECIFIC IMMUNOTHERAPY
;  FILE REFERENCE: 210121.465C4
;  CURRENT APPLICATION NUMBER: US/09/785,019
;  CURRENT FILING DATE:  2001-02-15
;  NUMBER OF SEQ ID NOS: 376
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 333
;   LENGTH: 410
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-785-019-333

  Query Match            98.2%;  Score 1418.5;  DB 10;  Length 410;
  Best Local Similarity  89.2%;  Pred. No. 1.5e-88;
  Matches  256;  Conservative    0;  Mismatches    0;  Indels   31;  Gaps    1;

Qy          1 MQHHHHHH------------------------------GSDVRDLNALLPAVPSLGGGG 29
              ||||||||                              ||||||||||||||||||||||
Db        124 MQHHHHHHVSIEGRASSGGSGLVPRGSSGSGDDDDKSSRGSDVRDLNALLPAVPSLGGGG 183

Qy         30 GCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPPPPPPPPPHSFIKQEPSWGGAE 89
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPPPPPPPPPHSFIKQEPSWGGAE 243

Qy         90 PHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQP 149
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 PHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQP 303

Qy        150 AIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYGC 209
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 AIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYGC 363

Qy        210 HTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQMNLGATLKG 256
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 HTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQMNLGATLKG 410


RESULT 12
US-10-125-635A-333
; Sequence 333, Application US/10125635A
; Publication No. US20030039635A1
; GENERAL INFORMATION:
;  APPLICANT: Gaiger, Alexander
;  APPLICANT:  Smithgall, Molly D.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Cheever, Martin A.
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Sutherland, R. Alec
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
;  TITLE OF INVENTION:  SPECIFIC IMMUNOTHERAPY
;  FILE REFERENCE: 210121.465C7
;  CURRENT APPLICATION NUMBER: US/10/125,635A
;  CURRENT FILING DATE:  2002-07-19
;  NUMBER OF SEQ ID NOS: 461
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 333
;   LENGTH: 410
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-125-635A-333

  Query Match            98.2%;  Score 1418.5;  DB 14;  Length 410;
  Best Local Similarity  89.2%;  Pred. No. 1.5e-88;
  Matches  256;  Conservative    0;  Mismatches    0;  Indels   31;  Gaps    1;

Qy          1 MQHHHHHH------------------------------GSDVRDLNALLPAVPSLGGGG 29
              ||||||||                              ||||||||||||||||||||||
Db        124 MQHHHHHHVSIEGRASSGGSGLVPRGSSGSGDDDDKSSRGSDVRDLNALLPAVPSLGGGG 183

Qy         30 GCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPPPPPPPPPHSFIKQEPSWGGAE 89
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPPPPPPPPPHSFIKQEPSWGGAE 243

Qy         90 PHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQP 149
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 PHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQP 303

Qy        150 AIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYGC 209
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 AIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYGC 363

Qy        210 HTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQMNLGATLKG 256
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 HTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQMNLGATLKG 410


RESULT 13
US-10-002-603-333
; Sequence 333, Application US/10002603
; Publication No. US20030095971A1
; GENERAL INFORMATION:
;  APPLICANT: Gaiger, Alexander
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Smithgall, Molly
;  APPLICANT:  Moulton, Gus
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Sleath, Paul R.
;  APPLICANT:  Mossman, Sally
;  APPLICANT:  Evans, Lawrence
;  APPLICANT:  Spies, A. Gregory
;  APPLICANT:  Boydston, Jeremy
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
;  TITLE OF INVENTION:  SPECIFIC IMMUNOTHERAPY
;  FILE REFERENCE: 210121.465C6
;  CURRENT APPLICATION NUMBER: US/10/002,603
;  CURRENT FILING DATE:  2001-10-30
;  NUMBER OF SEQ ID NOS: 413
;  SOFTWARE: FastSEQ for Windows Version 3.0
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; SEQ ID NO 333
;   LENGTH: 410
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-002-603-333

  Query Match             98.2%;  Score 1418.5;  DB 14;  Length 410;
  Best Local Similarity   89.2%;  Pred. No. 1.5e-88;
  Matches  256;  Conservative    0;  Mismatches    0;  Indels   31;  Gaps    1;

Qy          1 MQHHHHHH------------------------------GSDVRDLNALLPAVPSLGGGG 29
              ||||||||                              ||||||||||||||||||||||
Db        124 MQHHHHHHVSIEGRASSGGSGLVPRGSSGSGDDDDKSSRGSDVRDLNALLPAVPSLGGGG 183

Qy         30 GCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPPPPPPPPPHSFIKQEPSWGGAE 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPPPPPPPPPHSFIKQEPSWGGAE 243

Qy         90 PHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQP 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 PHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQP 303

Qy        150 AIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYGC 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 AIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYGC 363

Qy        210 HTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQMNLGATLKG 256
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 HTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQMNLGATLKG 410


RESULT 14
US-10-195-835-333
; Sequence 333, Application US/10195835
; Publication No. US20030198622A1
; GENERAL INFORMATION:
;  APPLICANT: Gaiger, Alexander
;  APPLICANT:  Smithgall, Molly D.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Cheever, Martin A.
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Sutherland, R. Alec
;  APPLICANT:  Mossman, Sally P.
;  APPLICANT:  Evans, Lawrence S.
;  APPLICANT:  Swanson, Ryan M.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
;  TITLE OF INVENTION:  SPECIFIC IMMUNOTHERAPY
;  FILE REFERENCE: 210121.465C8
;  CURRENT APPLICATION NUMBER: US/10/195,835
;  CURRENT FILING DATE:  2002-07-12
;  NUMBER OF SEQ ID NOS: 461
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 333
;   LENGTH: 410
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-195-835-333

  Query Match             98.2%;  Score 1418.5;  DB 14;  Length 410;
  Best Local Similarity   89.2%;  Pred. No. 1.5e-88;
  Matches  256;  Conservative    0;  Mismatches    0;  Indels   31;  Gaps    1;

Qy          1 MQHHHHHH------------------------------GSDVRDLNALLPAVPSLGGGG 29
              ||||||||                              ||||||||||||||||||||||
Db        124 MQHHHHHHVSIEGRASSGGSGLVPRGSSGSGDDDDKSSRGSDVRDLNALLPAVPSLGGGG 183

Qy         30 GCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPPPPPPPPPHSFIKQEPSWGGAE 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPPPPPPPPPHSFIKQEPSWGGAE 243

Qy         90 PHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQP 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 PHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQP 303

Qy        150 AIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYGC 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 AIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYGC 363

Qy        210 HTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQMNLGATLKG 256
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 HTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQMNLGATLKG 410


RESULT 15
US-10-286-333-333
; Sequence 333, Application US/10286333
; Publication No. US20030215458A1
; GENERAL INFORMATION:
;  APPLICANT: Gaiger, Alexander
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Jaya, No. US20030215458A1alie
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
;  TITLE OF INVENTION:  SPECIFIC IMMUNOTHERAPY
;  FILE REFERENCE: 210121.465C10
;  CURRENT APPLICATION NUMBER: US/10/286,333
;  CURRENT FILING DATE:  2002-10-30
;  NUMBER OF SEQ ID NOS: 506
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 333
;   LENGTH: 410
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-286-333-333

  Query Match             98.2%;  Score 1418.5;  DB 15;  Length 410;
  Best Local Similarity   89.2%;  Pred. No. 1.5e-88;
  Matches  256;  Conservative    0;  Mismatches    0;  Indels   31;  Gaps    1;

Qy          1 MQHHHHHH------------------------------GSDVRDLNALLPAVPSLGGGG 29
              ||||||||                              ||||||||||||||||||||||
Db        124 MQHHHHHHVSIEGRASSGGSGLVPRGSSGSGDDDDKSSRGSDVRDLNALLPAVPSLGGGG 183

Qy         30 GCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPPPPPPPPPHSFIKQEPSWGGAE 89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 GCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPPPPPPPPPHSFIKQEPSWGGAE 243

Qy         90 PHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQP 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 PHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQP 303

Qy        150 AIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYGC 209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 AIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYGC 363

Qy        210 HTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQMNLGATLKG 256
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 HTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQMNLGATLKG 410


Search completed: May 10, 2005, 18:56:54
Job time : 136 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 10, 2005, 18:35:45 ; Search time 39 Seconds
(without alignments)
631.577 Million cell updates/sec

Title: US-09-785-019B-335
Perfect score: 1444
Sequence: 1 MQHHHHHHGSDVRDLNALLP.....TSQLECMTWNQMNLGATLKG 256

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1386	96.0	449	2	A38080	Wilms tumor suscep
2	1340.5	92.8	448	2	S33926	Wilms' tumor prote
3	1329	92.0	449	2	A39692	Wilms' tumor prote
4	971.5	67.3	410	2	JC5046	Wilms' tumor suppr
5	161.5	11.2	2715	2	T13049	eyelid - fruit fly
6	159.5	11.0	1585	2	T31611	hypothetical prote
7	148.5	10.3	530	2	A45690	transactivator EBN
8	145.5	10.1	576	2	T36729	probable serine/th
9	143	9.9	1176	2	T49482	hypothetical prote
10	142.5	9.9	1201	2	G86441	unknown protein [i
11	142	9.8	903	2	T00074	hypothetical prote
12	141	9.8	1018	2	T43168	hypothetical prote
13	141	9.8	1259	2	T16038	hypothetical prote
14	141	9.8	1541	2	T02831	AAA protein L4171.
15	140.5	9.7	1357	2	T29265	hypothetical prote
16	140	9.7	1132	2	A35098	MHC class III hist
17	139	9.6	530	2	T48627	hypothetical prote
18	139	9.6	990	2	T14756	hypothetical prote
19	138	9.6	172	2	D41132	collagen-related p
20	137.5	9.5	1443	2	S05979	steroid hormone re
21	137	9.5	306	2	T09067	extensin-like prot
22	136.5	9.5	1048	2	T31425	C-terminal domain-
23	135.5	9.4	632	2	T02627	hypothetical prote
24	135	9.3	707	2	A46302	PTB-associated spl
25	135	9.3	1091	2	T13170	diaphanous protein
26	134.5	9.3	495	1	S31223	transcription fact
27	134	9.3	1184	2	G01763	atrophin-1 - human
28	133	9.2	684	2	A56154	Abl substrate ena
29	132	9.1	907	2	E96636	hypothetical prote
30	131.5	9.1	416	2	T34279	hypothetical prote
31	131.5	9.1	620	2	S06733	hydroxyproline-ric
32	131	9.1	1249	2	T14150	vesicle associated
33	130.5	9.0	186	2	C41132	collagen-related p
34	130.5	9.0	278	2	B39066	proline-rich prote
35	130.5	9.0	418	2	T15142	hypothetical prote
36	130.5	9.0	548	2	S52735	CW17R protein - mo
37	130	9.0	1171	2	T17454	diaphanous-related
38	129.5	9.0	1008	2	T04462	hypothetical prote
39	129.5	9.0	1069	2	D85383	hypothetical prote
40	129.5	9.0	1184	2	S50832	atrophin-1 - human
41	129.5	9.0	1400	2	T31555	hypothetical prote
42	129.5	9.0	1870	2	S37671	MHC class III hist
43	129	8.9	366	2	T26449	hypothetical prote
44	129	8.9	430	2	S66671	neuron-derived rec
45	129	8.9	605	1	QQBE3R	BVRF2 (EC-RF3) pro

ALIGNMENTS

RESULT 1
A38080
Wilms tumor susceptibility protein WT1 - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Jun-2000
C;Accession: A38080; S08273; A34673; I38504; I52811; I58315; A56411; S26286
R;Gessler, M.; Konig, A.; Bruns, G.A.
Genomics 12, 807-813, 1992
A;Title: The genomic organization and expression of the WT1 gene.
A;Reference number: A38080; MUID:92241883; PMID:1572653
A;Accession: A38080
A;Molecule type: DNA
A;Residues: 1-449 <GES1>
A;Cross-references: GB:X61631; GB:S99414; NID:g37981; PIDN:CAA43819.1; PID:g825731
A;Note: it is uncertain whether Met-1 is the initiator or whether translation is initiate
A;Note: sequence extracted from NCBI backbone (NCBIN:99414, NCBIN:99422, NCBIN:99479, NC
A;Note: the sequence in GenBank entry HSWTGEEX1, release 113.0, PIDN:CAA43819.1 differs
R;Gessler, M.; Poustka, A.; Cavenee, W.; Neve, R.L.; Orkin, S.H.; Bruns, G.A.P.
Nature 343, 774-778, 1990
A;Title: Homozygous deletion in Wilms tumours of a zinc-finger gene identified by chromo
A;Reference number: S08273; MUID:90158822; PMID:2154702
A;Accession: S08273
A;Molecule type: mRNA
A;Residues: 'SRQRPHPGALRNPTACPLPHFPPSLPPTHSPTHPPRAGTAAQAPGPRRLLAAILDFLLLQDPASTCVPEPASQHT
A;Cross-references: EMBL:X51630; NID:g37977; PIDN:CAA35956.1; PID:g37978
R;Call, K.M.; Glaser, T.; Ito, C.Y.; Buckler, A.J.; Pelletier, J.; Haber, D.A.; Rose, E.
Cell 60, 509-520, 1990
A;Title: Isolation and characterization of a zinc finger polypeptide gene at the human c
A;Reference number: A34673; MUID:90150277; PMID:2154335
A;Accession: A34673
A;Molecule type: mRNA
A;Residues: 85-249,267-364,'F',366-386,'T',388-407,411-449 <CAL>
A;Cross-references: GB:M30393; NID:g340381; PIDN:AAA36810.1; PID:g340382
R;Haber, D.A.; Sohn, R.L.; Buckler, A.J.; Pelletier, J.; Call, K.M.; Housman, D.E.
Proc. Natl. Acad. Sci. U.S.A. 88, 9618-9622, 1991
A;Title: Alternative splicing and genomic structure of the Wilms tumor gene WT1.
A;Reference number: A56411; MUID:92052142; PMID:1658787
A;Contents: annotation; alternative splicing
R;Phelan, S.A.; Lindberg, C.; Call, K.M.
Cell Growth Differ. 5, 677-686, 1994
A;Title: Wilms' tumor gene, WT1, mRNA is down-regulated during induction of erythroid an
A;Reference number: I38504; MUID:94368704; PMID:8086342
A;Accession: I38504
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-18 <PHE>
A;Cross-references: EMBL:U06486; NID:g473563; PIDN:AAA62865.1; PID:g458432
R;Pelletier, J.; Bruening, W.; Kashtan, C.E.; Mauer, S.M.; Manivel, J.C.; Striegel, J.E.
Cell 67, 437-447, 1991
A;Title: Germline mutations in the Wilms' tumor suppressor gene are associated with abno
A;Reference number: I52811; MUID:92005721; PMID:1655284
A;Accession: I52811

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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 355-365,'H',367-377 <PEL>
A;Cross-references: GB:S61513; NID:g237599; PIDN:AAB20109.1; PID:g237600
A;Note: mutant form
R;Hamilton, T.B.; Barilla, K.C.; Romaniuk, P.J.
Nucleic Acids Res. 23, 277-284, 1995
A;Title: High affinity binding sites for the Wilms' tumour suppressor protein WT1.
A;Reference number: I58315; MUID:95166649; PMID:7862533
A;Accession: I58315
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 'MGHHHHHHHHHHSSGHIEGRHM',301-364,'F',366-386,'T',388-407,411-449 <HAM>
A;Cross-references: GB:S75264; NID:g896246; PIDN:AAB33443.1; PID:g896247
A;Note: this sequence is engineered
C;Genetics:
A;Gene: GDB:WT1
A;Cross-references: GDB:120496; OMIM:194070
A;Map position: 11p13-11p13
A;Introns: 148/1; 189/1; 223/2; 249/2; 266/2; 298/3; 349/1; 379/1; 410/1
A;Note: mRNA transcripts containing both alternatively spliced regions are the most abun
C;Keywords: alternative splicing; DNA binding; kidney; tumor suppressor; zinc finger
F;1-449/Product: Wilms tumor susceptibility protein WT1, splice form 1 #status predicted
F;1-407,411-449/Product: Wilms tumor susceptibility protein WT1, splice form 4 #status p
F;1-249,267-449/Product: Wilms tumor susceptibility protein WT1, splice form 3 #status p
F;1-249,267-407,411-449/Product: Wilms tumor susceptibility protein WT1, splice form 2 #

  Query Match             96.0%;  Score 1386;  DB 2;  Length 449;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-84;
  Matches  248;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 61

Qy         69 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 121

Qy        129 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 181

Qy        189 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 241

Qy        249 NLGATLKG 256
              ||||||||
Db        242 NLGATLKG 249


RESULT 2
S33926
Wilms' tumor protein WT1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 10-May-1996
C;Accession: S33926
R;Sharma, P.M.; Yang, X.; Bowman, M.; Roberts, V.; Sukumar, S.
Cancer Res. 52, 6407-6412, 1992
A;Title: Molecular cloning of rat Wilms' tumor complementary DNA and a study of messenge
A;Reference number: S33926; MUID:93046155; PMID:1330293
A;Accession: S33926
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-448 <SHA>
A;Cross-references: EMBL:X69716
C;Genetics:
A;Gene: WT1
C;Keywords: tumor suppressor

  Query Match             92.8%;  Score 1340.5;  DB 2;  Length 448;
  Best Local Similarity   97.2%;  Pred. No. 1.5e-81;
  Matches  241;  Conservative    2;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          9 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 68
              |||||||||||||| |||||||| |||||| |||||||||||||||||||||||||| |
Db          2 GSDVRDLNALLPAVSSLGGGGGCGLPVSGARQWAPVLDFAPPGASAYGSLGGPAPPPA-P 60

Qy         69 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 128
              ||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||
Db         61 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTLHFSGQFTGTAGACRYGPFGPPPPSQAS 120

Qy        129 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 188
              ||||||||||||||||||||:|||||||||||| ||||||||||||||||||||||||||
Db        121 SGQARMFPNAPYLPSCLESQPSIRNQGYSTVTFDGAPSYGHTPSHHAAQFPNHSFKHEDP 180

Qy        189 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 240

Qy        249 NLGATLKG 256
              ||||||||
Db        241 NLGATLKG 248


RESULT 3
A39692
Wilms' tumor protein analog, WT1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 16-Feb-1997
C;Accession: A39692
R;Buckler, A.J.; Pelletier, J.; Haber, D.A.; Glaser, T.; Housman, D.E.
Mol. Cell. Biol. 11, 1707-1712, 1991
A;Title: Isolation, characterization, and expression of the murine Wilms' tumor gene (WT1
A;Reference number: A39692; MUID:91141522; PMID:1671709
A;Accession: A39692
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-449 <BUC>
A;Cross-references: GB:M55512
C;Keywords: alternative splicing; DNA binding; transcription regulation; tumor suppressor

  Query Match             92.0%;  Score 1329;  DB 2;  Length 449;
  Best Local Similarity   96.8%;  Pred. No. 8.7e-81;
  Matches  241;  Conservative    1;  Mismatches    5;  Indels    2;  Gaps    2;

Qy          9 GSDVRDLNALLPAVPSL-GGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAP 67
              |||||||||||||| || |||||| |||||| ||||||||||||||||||||||||||
Db          2 GSDVRDLNALLPAVSSLGGGGGGCGLPVSGARQWAPVLDFAPPGASAYGSLGGPAPPPA- 60

Qy         68 PPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQA 127
              ||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||
Db         61 PPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTLHFSGQFTGTAGACRYGPFGPPPPSQA 120

Qy        128 SSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHED 187
              |||||||||||||||||||| |||||||||||| |||||||||||||||||||||||||
Db        121 SSGQARMFPNAPYLPSCLESQPTIRNQGYSTVTFDGAPSYGHTPSHHAAQFPNHSFKHED 180

Qy        188 PMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQ 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQ 240

Qy        248 MNLGATLKG 256
              |||||||||
Db        241 MNLGATLKG 249


RESULT 4
JC5046
Wilms' tumor suppressor protein - African clawed frog
N;Alternate names: WT1
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004
C;Accession: JC5046
R;Semba, K.; Saito-Ueno, R.; Takayama, G.; Kondo, M.
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Gene 175, 167-172, 1996
A;Title: cDNA cloning and its pronephros-specific expression of the Wilms' tumor suppres
A;Reference number: JC5046; MUID:97074667; PMID:8917094
A;Contents: testis
A;Accession: JC5046
A;Molecule type: mRNA
A;Residues: 1-410 <SEM>
A;Cross-references: UNIPROT:P79958; DDBJ:D82051
C;Comment: This protein is involved in kidney morphogenesis.
C;Genetics:
A;Gene: wt1

  Query Match             67.3%;  Score 971.5;  DB 2;  Length 410;
  Best Local Similarity   73.7%;  Pred. No. 3.1e-57;
  Matches  182;  Conservative   19;  Mismatches   23;  Indels   23;  Gaps    6;

Qy          9 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 68
              |||||||:| ||| | || |    | :||| ::|||||||| ||||  | ||
Db          2 GSDVRDMN-LLPPVSSLSGNSSCNMPVSNSSQWAPVLDF-PPGA-PYSSL---------- 48

Qy         69 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 128
                  |||||||||:|    :|||:|||||||||||||||||||||||| | ||||:
Db         49 -----TPHSFIKQEPTW-NPDPHEDQCLSAFTVHFSGQFTGTAGACRYGPFGAPTPSQAT 102

Qy        129 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 188
              :|||||||||||| :||::| ::|||||| | ||||||||||||| ||| |||||||||
Db        103 TGQARMFPNAPYLSNCLDNQQSMRNQGYSAVAFDGTPSYGHTPSHHTAQFTNHSFKHEDP 162

Qy        189 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 248
              : || |||||||||||||||||||:|||||||||||||:|||||||    ||||||||
Db        163 ISQQTSLGEQQYSVPPPVYGCHTPTDTCTGSQALLLRTPYNSDNLYQM----ECMTWNQM 218

Qy        249 NLGATLK 255
              |||::||
Db        219 NLGSSLK 225


RESULT 5
T13049
eyelid - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13049
R;Treisman, J.E.; Luk, A.; Rubin, G.M.; Heberlein, U.
submitted to the EMBL Data Library, March 1998
A;Reference number: Z17592
A;Accession: T13049
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2715 <TRE>
A;Cross-references: UNIPROT:Q8IN94; EMBL:AF053091; NID:g2981220; PID:g2981221; PIDN:AAC0
C;Genetics:
A;Gene: eld
A;Cross-references: FlyBase:FBgn0003013
C;Function:
A;Description: could act as a transcription factor antagonistic to the Wg pathway
C;Keywords: DNA binding

  Query Match             11.2%;  Score 161.5;  DB 2;  Length 2715;
  Best Local Similarity   26.3%;  Pred. No. 0.006;
  Matches   67;  Conservative   17;  Mismatches   84;  Indels   87;  Gaps   12;

Qy         23 PSLGGGGGCALPVSGAAQ---WAPVLDFAPPGASAYGSLGGPAPPPAPPPPPPPPHSFI 79
              |  |||    | ||       |    | || | |::||    | | ||||  ||:
Db       1217 PIAAGGG----PGSGTGPGPGQGPGPGAASGGAGAVGAVGG---GPQPHPPPPHSPHTAA 1269

Qy         80 KQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFP--- 136
              :|      |  |::|       |    |  |          |||||  |    | :  |
Db       1270 QQ-----AAGQHQQQ-------HPQHQHPGLP--------GPPPPQQQQGQQGQQPPPSV 1309

Qy        137 ----------------------------NAPYLP-------------SCLESQPAIRNQ 154
                                         ||| |              |   |||    |
Db       1310 GGGPPPAPQQHGPGQVPPSPQQHVRPAAGAPYPPGGSGYPTPVSRTPGSPYPSQPGAYGQ 1369

Qy        155 GYSTVTFDGT----PSYGHTPSHHAAQ----FPNHSFKHEDP---MGQQGSLGEQQYSVP 203
                |:  :: |       :|  |  :  |     :| :  : | |      | |  | : || |
Db       1370 YGSSDQYNATGPPGQPFGQGPGQYPPQNRNMYPPYGPEGEAPPTGANQYGPYGSRPYSQP 1429

Qy        204 PPVYGCHTPTDSCTG 218
              ||  |   || :  |
Db       1430 PP-GGPQPPTQTVAG 1443


RESULT 6
T31611
hypothetical protein Y50E8A.g - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T31611
R;Steward, C.
submitted to the EMBL Data Library, September 1999
A;Reference number: Z21047
A;Accession: T31611
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1585 <WIL>
A;Cross-references: EMBL:AL117200; NID:e1549770; PIDN:CAB55050.1; CESP:Y50E8A.g
A;Experimental source: clone Y50E8A
C;Genetics:
A;Gene: CESP:Y50E8A.g
A;Introns: 25/3; 60/1; 133/2; 217/3; 270/3; 337/2; 400/1; 746/2

  Query Match             11.0%;  Score 159.5;  DB 2;  Length 1585;
  Best Local Similarity   29.5%;  Pred. No. 0.0047;
  Matches   54;  Conservative   14;  Mismatches   72;  Indels   43;  Gaps    6;

Qy         26 GGGGGCALPVSGAAQWAPVLDFAP-----PGASAY--------------GSLGG-----P 61
              ||||| :   || :   |    ||      | :  |              || ||
Db       1417 GGGGGSSGGYSGGSAAPPPPPPAPAPAPAPSSGGYSGGSSGGSAAGGGGGSSGGYTGGSA 1476

Qy         62 APPPAPPPPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGP 121
              |||| |||||||||       || ||          :|      |   |::|    |   |
Db       1477 APPPPPPPPPPPPPAPAPAPAPSSGGYSGGSSGGSAA------GGGGGSSGGYTGGSAAP 1530

Qy        122 PPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPS---YGHTPSHHAAQF 178
              |||           |  |  |       ||  : |||  :  |: :     | :  :  ::|
Db       1531 PPPP----------PPPPPPPPAPAPAPAPSSGGYSGGSSGGSAAGGGGGSSGGYSGSRF 1580

Qy        179 PNH 181
              |
Db       1581 ARH 1583


RESULT 7
A45690
transactivator EBNA-2 - baboon lymphotropic virus
C;Species: baboon lymphotropic virus, herpesvirus papio HVP
C;Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: A45690
R;Ling, P.D.; Ryon, J.J.; Hayward, S.D.
J. Virol. 67, 2990-3003, 1993
A;Title: EBNA-2 of herpesvirus papio diverges significantly from the type A and type B E
ic motif.
A;Reference number: A45690; MUID:93267743; PMID:8388484
A;Accession: A45690
A;Molecule type: DNA
A;Residues: 1-530 <LIN>
A;Cross-references: UNIPROT:Q07701; GB:L11366; NID:g6690013; PIDN:AAA79034.1; PID:g30631
A;Note: sequence extracted from NCBI backbone (NCBIN:132361, NCBIP:132362)
C;Superfamily: hydroxyproline-rich glycoprotein

  Query Match             10.3%;  Score 148.5;  DB 2;  Length 530;
  Best Local Similarity   25.4%;  Pred. No. 0.0084;
  Matches   68;  Conservative   20;  Mismatches   95;  Indels   85;  Gaps   12;

Qy         18 LLPAVPSLGGGGGCALPVSGAAQWAPVLDF-----------AP-PGASAYGSLGGPAPP 64
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Db         30 LTPTVPALG-------PLSE----APLIPLKIIVGESSDQHQGPLPGPSNLPPPSPPPPP 78

Qy         65 PAPPPPPPPPPPHSFIKQEPSWGGAEPHEEQ-----------------CLSAFTVHFSGQ 106

Db         79 PPPPPPPPPPPPQPERRDAATQEPDPHDIRPLGISPENGALASAIRMLCMSSYIVR---- 134

Qy        107 FTGTAGAC-----RYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTF 161

Db        135 --QTQGACGLLNPRVKPRVPRP---------RMTILRPLTPLRLIRPP---RPTYNPLSS 180

Qy        162 DGTPSYGHTPSHHAAQFP---------NHSFKHE---DPMGQQGSLGEQQYSVPPPVYGC 209

Db        181 PNTPSPSPIPFQHTPLPPRPPTASPPHSHPFQSEPKQTPPKPTLPLPGPPVSPPPPTPSI 240

Qy        210 H--------TPTDSCTGSQALLLRTPYS 229

Db        241 QPTPHPTPPKPTIPSSGPHITLTPVPLS 268


RESULT 8
T36729
probable serine/threonine-specific protein kinase (EC 2.7.1.-) - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2004
C;Accession: T36729
R;Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1999
A;Reference number: Z21612
A;Accession: T36729
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-576 <MUR>
A;Cross-references: UNIPROT:Q9XA04; EMBL:AL079308; PIDN:CAB45227.1; GSPDB:GN00070; SCOED
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCH69.30
C;Superfamily: protein kinase homology
C;Keywords: phosphotransferase; serine/threonine-specific protein kinase

  Query Match             10.1%;  Score 145.5;  DB 2;  Length 576;
  Best Local Similarity   28.3%;  Pred. No. 0.014;
  Matches   53;  Conservative   18;  Mismatches   69;  Indels   47;  Gaps   11;

Qy         49 PPGASAYGSLGGPAPPPAPPPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFT 108

Db        313 PPGVD-------PSPPATPPTPPPAPP---------WQGTPP-------------AGP-- 341

Qy        109 GTAGACRYGPFGP-PPPSQASSGQARMFPNAPYLPSCLESQPAI---RNQGYSTVTFDG- 163

Db        342 -SSGLDRPSPGSPGPPPTGPDSTPASPPPGTPVTATGTPSAPGLPPASDQGWTPSTPSGP 400

Qy        164 --TPSYGHTPSHHAAQFPNHSFKH-----EDPMGQQ-GSLGEQ-QYSVPPPVYGCHTPTD 214

Db        401 TAPPSAPSAPSAPSAPGPTRPAPHGTHSEEVPLAERPGAMSETGSFHLPPP-QPTVTPTS 459

Qy        215 SCTGSQA 221

Db        460 DAAASDA 466


RESULT 9
T49482
hypothetical protein B14D6.340 [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T49482
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
A;Accession: T49482
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1176 <SCH>
A;Cross-references: UNIPROT:Q8WZK9; EMBL:AL356173; GSPDB:GN00116; NCSP:B14D6.340
A;Experimental source: BAC clone B14D6; strain OR74A
C;Genetics:
A;Gene: NCSP:B14D6.340
A;Map position: 6
F;207-245/Domain: GAL4 zinc binuclear cluster homology <GL4>

  Query Match             9.9%;  Score 143;  DB 2;  Length 1176;
  Best Local Similarity   24.9%;  Pred. No. 0.043;
  Matches   62;  Conservative   20;  Mismatches   97;  Indels   70;  Gaps    9;

Qy         17 ALLPAVPSLGG----------GGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGP----- 61

Db        907 AQVPMVPSTSSQTPTSATRPTHSLASTPTSATAPPPPYSQGPPPPVTVSGPHPPPPPPVH 966

Qy         62 ----APPPAPPPPPPPPPHSFIKQEP--------------SWGGAE-----PHEEQCLS 97

Db        967 YSHHAPPPPPPPPPPPPPSARGRQMPPIQPGPSPQQPPPPASWGHPTSGPTLPPPQQARS 1026

Qy         98 AFTVHFSGQFTGTAGACRYGPFGPPPPSQ---------ASSGQARMFPNAPYLPSCLESQ 148

Db       1027 PYIPPHA-----------HHPQGPPPPAQPPTLPSISPAGTPRIKSEPGLPSLPPLGGDR 1075

Qy        149 PAIRNQGYSTVTFDG---TPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVP-P 204

Db       1076 DDKRPIGLGIGGGGGGERGPASAISPSNRAAVL-------QSSVGGGHGAGSPTLSVSRS 1128

Qy        205 PVYGCHTPT 213

Db       1129 PISATTTPT 1137


RESULT 10
G86441
unknown protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: G86441
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: G86441
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1201 <STO>
A;Cross-references: UNIPROT:Q9C6S1; GB:AE005172; NID:g11136725; PIDN:AAG31306.1; GSPDB:GN
C;Genetics:
A;Map position: 1

  Query Match             9.9%;  Score 142.5;  DB 2;  Length 1201;
  Best Local Similarity   25.6%;  Pred. No. 0.047;
  Matches   60;  Conservative   15;  Mismatches   86;  Indels   73;  Gaps   10;

Qy          4 HHHHHGSDVRD-----LNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPP---GASAY 55

Db        449 HHHHHEIPAKDSVDNPLN--LPSDPPSSGDHVTLLP-------PPPPPPPPLFTSTTSF 499

Qy         56 GSLGGPAPPPAPP-----------PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAF---- 99

Db        500 SPSQPPPPPPPPPLFMSTTSFSPSQPPPPPPPPPLFTSTTSFSPSQPPPPPPLPSFSNRD 559

Qy        100 ---TVHFSGQFTGTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPS-----CLESQPAI 151

Db        560 PLTTLHQPINKT-----------PPPPP----------PPPPPLPSRSIPPPLAQPPPP 597
```

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Qy        152 RNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPP 205
              |           |      ||  :   |:       |    || | :: : |||
Db        598 R----------PPPPPPPPPSSRSIPSPSAPPPPPPPPPSFGSTGNKRQAQPPP 641


RESULT 11
T00074
hypothetical protein KIAA0460 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C;Accession: T00074
R;Seki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura, N.;
DNA Res. 4, 345-349, 1997
A;Title: Characterization of cDNA clones in size-fractionated cDNA libraries from human
A;Reference number: Z14085; MUID:98116662; PMID:9455484
A;Accession: T00074
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-903 <SEK>
A;Cross-references: UNIPROT:O75048; EMBL:AB007929; NID:g3413881; PIDN:BAA32305.1; PID:g3
A;Experimental source: brain
C;Genetics:
A;Note: KIAA0460

  Query Match             9.8%;  Score 142;  DB 2;  Length 903;
  Best Local Similarity   25.5%;  Pred. No. 0.038;
  Matches   61;  Conservative   18;  Mismatches   98;  Indels   62;  Gaps    7;

Qy          7 HHGSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPA 66
              | |   ||    ||:|         : | :  |  |       |||   :  :  | |||
Db        665 HGGIFSRDAPTHLPSV-------DLSNPFTKEAALAHAAPPPPPG--EHSGIPFPTPPPP 715

Qy         67 PP---------------PPPPPPP--HSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFT 108
              ||               |||||||  || :   |:   ||      :: |    |
Db        716 PPPGEHSSSGGSGVPFSTPPPPPPPVDHSGVVPFPAPPLAEHGVAGAVAVFPKDHSSLLQ 775

Qy        109 GTAGACRYGPFGPPPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYG 168
              ||        ||  |  :   |  :   | | |    ||
Db        776 GTLAE----HFGVLPGPRDHGGPTQRDLNGPGLSRVRES---------------------- 810

Qy        169 HTPSHHAAQFPNHSFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTP 227
                  |:|| :|  |     |  |     |  ||:   |  | | :|   ::||:|
Db        811 -------LTLPSHSLEHLGPPHGGGGGGGSNSSSGPPLGPSHRDTISRSG---IILRSP 859


RESULT 12
T43168
hypothetical protein cyk-1 - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C;Accession: T43168
R;Swan, K.A.; Severson, A.F.; Carter, J.C.; Martin, P.R.; Schnabel, H.; Schnabel, R.; Bo
J. Cell Sci. 111, 2017-2027, 1998
A;Title: cyk-1: a C. elegans FH gene required for a late step in embryonic cytokinesis.
A;Reference number: Z22311; MUID:98311662; PMID:9645949
A;Accession: T43168
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1018 <SWA>
A;Cross-references: UNIPROT:O61701; EMBL:AF062008; PIDN:AAC17501.1
C;Genetics:
A;Gene: cyk-1
A;Map position: 3

  Query Match             9.8%;  Score 141;  DB 2;  Length 1018;
  Best Local Similarity   31.5%;  Pred. No. 0.05;
  Matches   45;  Conservative    6;  Mismatches   42;  Indels   50;  Gaps    8;

Qy         21 AVPSLGGGGGCAL-PVSGA---AQWAPVLDFAPPGASAYGSL----GGPAPPPAP----- 67
              : ||   ||  || |::|        | :   ||      | |    ||| ||| |
Db        277 SAPSTSAGGSSALPPITGGPPPPPGLPPITGGPPPPPPPGGLPPITGGPPPPPPPGGLPP 336

Qy         68 ----PPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPP 123
                  ||||||||           ||  |                    |  : ||  |||
Db        337 ISGGPPPPPPPP----------GGCPPPPP--------------PPPPGGFKGGPPPPPP 372

Qy        124 PSQASSGQARMF-PNAPYLPSCL 145
              |         || | || :|  |
Db        373 PG--------MFAPMAPVIPDYL 387


RESULT 13
T16038
hypothetical protein F11H8.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16038
R;Menezes, S.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid F11H8.
A;Reference number: Z18450
A;Accession: T16038
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1259 <MEN>
A;Cross-references: UNIPROT:Q95ZV4; EMBL:U40187; NID:g1055194; PID:g1055198; PIDN:AAA811
C;Genetics:
A;Gene: CESP:F11H8.4
A;Introns: 160/3; 192/1; 212/3; 291/3; 350/3; 417/2; 511/3; 632/1; 677/3; 895/1; 1073/2;

  Query Match             9.8%;  Score 141;  DB 2;  Length 1259;
  Best Local Similarity   31.5%;  Pred. No. 0.062;
  Matches   45;  Conservative    6;  Mismatches   42;  Indels   50;  Gaps    8;

Qy         21 AVPSLGGGGGCAL-PVSGA---AQWAPVLDFAPPGASAYGSL----GGPAPPPAP----- 67
              : ||   ||  || |::|        | :   ||      | |    ||| ||| |
Db        694 SAPSTSAGGSSALPPITGGPPPPPGLPPITGGPPPPPPPGGLPPITGGPPPPPPPGGLPP 753

Qy         68 ----PPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPP 123
                  ||||||||           ||  |                    |  : ||  |||
Db        754 ISGGPPPPPPPP----------GGCPPPPP--------------PPPPGGFKGGPPPPPP 789

Qy        124 PSQASSGQARMF-PNAPYLPSCL 145
              |         || | || :|  |
Db        790 PG--------MFAPMAPVIPDYL 804


RESULT 14
T02831
AAA protein L4171.3 [imported] - Leishmania major (strain Friedlin)
C;Species: Leishmania major
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: C81460; T02831
R;Myler, P.J.; Audleman, L.; deVos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C.;
Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
A;Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protein-c
A;Reference number: A81455; MUID:99178987; PMID:10077609
A;Accession: C81460
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1541 <PYL>
A;Cross-references: UNIPROT:O15837; GB:AE001274; NID:g3264850; PIDN:AAC24654.1; PID:g226
A;Experimental source: strain MHOM/IL/81/Friedlin
C;Genetics:
A;Gene: L4171.3
A;Map position: 1

  Query Match             9.8%;  Score 141;  DB 2;  Length 1541;
  Best Local Similarity   26.8%;  Pred. No. 0.076;
  Matches   61;  Conservative   14;  Mismatches  105;  Indels   48;  Gaps   10;

Qy         27 GGGGCALPVSGAAQWAPVLDFA---------------------------PPGASAYG-- 56
              | |    | |||    ||    |                           |||:: |
Db         90 GTGTKGSPASGAQTLAPPAQSAGKKSMMMMMPPPPRFPPEMAGMVPGMPPPMPGAASTGGM 149
```

```
Qy          57 -SLGGPAPPPAPPPPPP---PPPHSFIKQEPSWGGAEPHEEQCLSAFT--VHFSGQFTGT 110
Db         150 MSAGFMPPPPPPPPPPPMMMPPLNGMIFQPPGTPGMPHHHHHPAGMATPQQHLASQHQHQ 209

Qy         111 AGACRYGPFGPPPPSQASSGQAR----MFPNAPYLPSCLESQPAIRNQGYSTVTF-DGTP 165
Db         210 HQHGMMPMWMPPPPTQTQQHQQQQPGMMMPMNSMMPM---SMPMSMPMGAASSPLPPGQH 266

Qy         166 SYGHTPSHHAAQFPNHSFK-HEDPMGQQGSLGEQQYSVPPPVYGCHTP 212
Db         267 SSG--PQQHPPQQPGMMMPFYPPPQAPHGTM-PPMASMPPPAPGMGVP 311


RESULT 15
T29265
hypothetical protein C01G8.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T29265
R;Du, Z.; Gattung, S.
submitted to the EMBL Data Library, November 1996
A;Description: The sequence of C. elegans cosmid C01G8.
A;Reference number: Z20597
A;Accession: T29265
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1357 <DUZ>
A;Cross-references: EMBL:U80439; PIDN:AAB37645.1; GSPDB:GN00019; CESP:C01G8.7
A;Experimental source: strain Bristol N2; clone C01G8
C;Genetics:
A;Gene: CESP:C01G8.7
A;Map position: 1
A;Introns: 89/1; 488/1; 701/3; 1056/2; 1159/3; 1197/1; 1312/3

  Query Match              9.7%;  Score 140.5;  DB 2;  Length 1357;
  Best Local Similarity   22.3%;  Pred. No. 0.073;
  Matches   62;  Conservative   17;  Mismatches   72;  Indels  127;  Gaps   14;

Qy          20 PAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAY---------------------- 55
Db         364 PGYPGYGPPGAMRPPAG----------FAPPPGAPYGYPPGAPPPAGFHPSHPQHPQHAQ 413

Qy          56 ---------------------GSLGGPAPP------PAPPPPP----PPPPHSFIKQEPS 84
Db         414 YLAWQQQRYHQQQQHQQQQQQGAPGGPRPPYPYPGGPVPPGPPQNRMPPPP-------PA 466

Qy          85 WGGAEPHEEQCLSAFTVHFSGQFTGTAGA----CRYGPFGPPPPSQASSGQAR-MFPNAP 139
Db         467 QGAPSP-----------------SGAAGSNGKQPRYGT--PAPPSRASAPTPQPLSSTMP 507

Qy         140 YLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPS------HHAAQFPNHSFKHEDPMGQQG 193
Db         508 VVAPSTSTQPTPTTGSYLANTL-ATPGPAHAPSSSMSHAHHV------------------ 548

Qy         194 SLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSD 231
Db         549 -ISQQQHQYPP---GCIEAT--ATSQNQVKRRKVYARE 580


Search completed: May 10, 2005, 18:45:33
Job time : 40 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 10, 2005, 18:27:44 ; Search time 173 Seconds
(without alignments)
757.759 Million cell updates/sec

Title: US-09-785-019B-335
Perfect score: 1444
Sequence: 1 MQHHHHHHGSDVRDLNALLP.....TSQLECMTWNQMNLGATLKG 256

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1386	96.0	249	2	Q6PI38	Q6pi38 homo sapien
2	1386	96.0	449	1	WT1_HUMAN	P19544 homo sapien
3	1367	94.7	449	1	WT1_PIG	O62651 sus scrofa
4	1340.5	92.8	448	1	WT1_RAT	P49952 rattus norv
5	1329	92.0	449	1	WT1_MOUSE	P22561 mus musculu
6	1094.5	75.8	414	2	Q9I8A1	Q9i8a1 gallus gall
7	1094.5	75.8	417	2	Q9I8A0	Q9i8a0 gallus gall
8	1089.5	75.5	392	2	Q91030	Q91030 gallus gall
9	971.5	67.3	407	2	P79958	P79958 xenopus lae
10	957.5	66.3	390	2	O42223	O42223 trachemys s
11	940.5	65.1	409	2	Q91657	Q91657 xenopus lae
12	933	64.6	426	2	Q9W611	Q9w611 cynops pyrr
13	845.5	58.6	419	2	Q9PUT7	Q9put7 brachydanio
14	822	56.9	417	2	Q90XX6	Q90xx6 oncorhynchu
15	776	53.7	386	2	Q90XX8	Q90xx8 oncorhynchu
16	769	53.3	250	2	Q98SJ4	Q98sj4 brachydanio
17	733	50.8	392	2	Q9IBF0	Q9ibf0 anguilla ja
18	728.5	50.5	388	2	Q90XX7	Q90xx7 oncorhynchu
19	715.5	49.5	410	2	Q8JIR9	Q8jir9 oryzias lat
20	713.5	49.4	418	2	Q90XX4	Q90xx4 oncorhynchu
21	707.5	49.0	418	2	Q90XX5	Q90xx5 oncorhynchu
22	629	43.6	416	2	O93433	O93433 fugu rubrip
23	525	36.4	288	1	WT1_ALLMI	P50902 alligator m
24	407	28.2	251	2	Q866X3	Q866x3 ovis aries
25	306	21.2	239	1	WT1_SMIMA	P49953 sminthopsis
26	235	16.3	42	2	O18760	O18760 sus scrofa
27	168.5	11.7	431	2	Q9PVG9	Q9pvg9 coturnix co
28	168	11.6	2058	2	Q7PUR9	Q7pur9 anopheles g
29	166.5	11.5	659	2	Q6C7Q8	Q6c7q8 yarrowia li
30	161.5	11.2	2716	1	OSA_DROME	Q8in94 drosophila
31	153.5	10.6	993	2	Q9VY31	Q9vy31 drosophila
32	153	10.6	812	2	Q8LJ56	Q8lj56 oryza sativ
33	149.5	10.4	371	2	Q9BHV7	Q9bhv7 leishmania
34	148.5	10.3	530	2	Q07701	Q07701 herpesvirus
35	147.5	10.2	594	2	Q9VEP4	Q9vep4 drosophila
36	147	10.2	451	2	Q62775	Q62775 rattus norv
37	146	10.1	548	2	Q6DDW4	Q6ddw4 xenopus lae
38	146	10.1	615	2	Q6EU15	Q6eu15 oryza sativ
39	146	10.1	917	2	Q873D8	Q873d8 neurospora
40	145.5	10.1	576	2	Q9XA04	Q9xa04 streptomyce
41	145.5	10.1	906	2	Q6MWG9	Q6mwg9 oryza sativ
42	145	10.0	313	2	Q8L556	Q8l556 oryza sativ
43	144.5	10.0	447	2	O73628	O73628 anolis caro
44	144.5	10.0	639	2	Q9NVZ9	Q9nvz9 homo sapien
45	144	10.0	384	2	Q6VFT5	Q6vft5 oryctolagus

ALIGNMENTS

RESULT 1
Q6PI38
ID Q6PI38 PRELIMINARY; PRT; 249 AA.
AC Q6PI38;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE WT1 protein.
GN Name=WT1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC046461; AAH46461.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000976; Wilms_tumour.
DR Pfam; PF02165; WT1; 1.
DR PRINTS; PR00049; WILMSTUMOUR.
SQ SEQUENCE 249 AA; 25967 MW; 33F53B96A79CBF28 CRC64;

Query Match 96.0%; Score 1386; DB 2; Length 249;
Best Local Similarity 100.0%; Pred. No. 1.1e-77;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          9 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 61

Qy         69 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 121

Qy        129 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 181

Qy        189 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 241

Qy        249 NLGATLKG 256
              ||||||||
Db        242 NLGATLKG 249
```

RESULT 2
WT1_HUMAN
ID WT1_HUMAN STANDARD; PRT; 449 AA.
AC P19544; Q15881; Q16256; Q16575; Q8IYZ5;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Wilms' tumor protein (WT33).
GN Name=WT1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal kidney;
RX MEDLINE=90158822; PubMed=2154702; DOI=10.1038/343774a0;
RA Gessler M., Poustka A., Cavenee W., Neve R.L., Orkin S.H.,
RA Bruns G.A.P.;
RT "Homozygous deletion in Wilms tumours of a zinc-finger gene identified
RT by chromosome jumping.";
RL Nature 343:774-778(1990).
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Placenta;
RX MEDLINE=92052142; PubMed=1658787;
RA Haber D.A., Sohn R.L., Buckler A.J., Pelletier J., Call K.M.,
RA Housman D.E.;
RT "Alternative splicing and genomic structure of the Wilms tumor gene
RT WT1.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:9618-9622(1991).
RN [3]
RP SEQUENCE FROM N.A.
RA Frankland J.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 4).
RX MEDLINE=92241883; PubMed=1572653;
RA Gessler M., Konig A., Bruns G.A.P.;
RT "The genomic organization and expression of the WT1 gene.";
RL Genomics 12:807-813(1992).
RN [5]
RP SEQUENCE FROM N.A.
RA Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RT "NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department
RT of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
RN [6]
RP SEQUENCE OF 85-449 FROM N.A.
RX MEDLINE=90150277; PubMed=2154335; DOI=10.1016/0092-8674(90)90601-A;
RA Call K.M., Glaser T., Ito C.Y., Buckler A.J., Pelletier J.,
RA Haber D.A., Rose E.A., Kral A., Yeger H., Lewis W.H., Jones C.,
RA Housman D.E.;
RT "Isolation and characterization of a zinc finger polypeptide gene at
RT the human chromosome 11 Wilms' tumor locus.";
RL Cell 60:509-520(1990).
RN [7]
RP SEQUENCE OF 148-449 FROM N.A. (ISOFORM 4).
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP SEQUENCE OF 301-449 FROM N.A.
RC TISSUE=Fetal kidney;
RX MEDLINE=95166649; PubMed=7862533;
RA Hamilton T.B., Barilla K.C., Romaniuk P.J.;
RT "High affinity binding sites for the Wilms' tumour suppressor protein
RT WT1.";
RL Nucleic Acids Res. 23:277-284(1995).
RN [9]
RP IDENTIFICATION OF START CODON AND ALTERNATIVE SPLICE SITES.
RX MEDLINE=91141522; PubMed=1671709;
RA Buckler A.J., Pelletier J., Haber D.A., Glaser T., Housman D.E.;
RT "Isolation, characterization, and expression of the murine Wilms'
RT tumor gene (WT1) during kidney development.";
RL Mol. Cell. Biol. 11:1707-1712(1991).
RN [10]
RP INTERACTION WITH WTAP.
RX MEDLINE=20458888; PubMed=11001926;
RA Little N.A., Hastie N.D., Davies R.C.;
RT "Identification of WTAP, a novel Wilms' tumour 1-associating
RT protein.";
RL Hum. Mol. Genet. 9:2231-2239(2000).
RN [11]
RP INTERACTION WITH ZNF224.
RX PubMed=12239212; DOI=10.1074/jbc.M205667200;
RA Lee T.H., Lwu S., Kim J., Pelletier J.;
RT "Inhibition of Wilms tumor 1 transactivation by bone marrow zinc
RT finger 2, a novel transcriptional repressor.";
RL J. Biol. Chem. 277:44826-44837(2002).
RN [12]
RP REVIEW.
RX MEDLINE=92207913; PubMed=1313285;
RA Haber D.A., Buckler A.J.;
RT "WT1: a novel tumor suppressor gene inactivated in Wilms' tumor.";
RL New Biol. 4:97-106(1992).
RN [13]
RP REVIEW.
RX MEDLINE=93345769; PubMed=8393820;
RA Rauscher F.J. III;
RT "The WT1 Wilms tumor gene product: a developmentally regulated
RT transcription factor in the kidney that functions as a tumor
RT suppressor.";

```
RL   FASEB J. 7:896-903(1993).
RN   [14]
RP   VARIANT WT1 CYS-366.
RX   MEDLINE=92279213; PubMed=1317572;
RA   Little M.H., Prosser J., Condie A., Smith P.J., van Heyningen V.,
RA   Hastie N.D.;
RT   "Zinc finger point mutations within the WT1 gene in Wilms tumor
RT   patients.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:4791-4795(1992).
RN   [15]
RP   VARIANTS DDS.
RX   MEDLINE=92005721; PubMed=1655284; DOI=10.1016/0092-8674(91)90194-4;
RA   Pelletier J., Bruening W., Kashtan C.E., Mauer S.M., Manivel J.C.,
RA   Striegel J.E., Houghton D.C., Junien C., Habib R., Fouser L.,
RA   Fine R.N., Silverman B.L., Haber D.A., Housman D.E.;
RT   "Germline mutations in the Wilms' tumor suppressor gene are associated
RT   with abnormal urogenital development in Denys-Drash syndrome.";
RL   Cell 67:437-447(1991).
RN   [16]
RP   VARIANTS DDS.
RX   MEDLINE=93265053; PubMed=1338906;
RA   Baird P.N., Santos A., Groves N., Jadresic L., Cowell J.K.;
RT   "Constitutional mutations in the WT1 gene in patients with Denys-Drash
RT   syndrome.";
RL   Hum. Mol. Genet. 1:301-305(1992).
RN   [17]
RP   SEQUENCE OF 385-405 FROM N.A., AND VARIANT DDS TRP-394.
RX   MEDLINE=93250986; PubMed=1302008;
RA   Bruening W., Bardeesy N., Silverman B.L., Cohn R.A., Machin G.A.,
RA   Aronson A.J., Housman D., Pelletier J.;
RT   "Germline intronic and exonic mutations in the Wilms' tumour gene
RT   (WT1) affecting urogenital development.";
RL   Nat. Genet. 1:144-148(1992).
RN   [18]
RP   VARIANTS DDS.
RX   MEDLINE=93271983; PubMed=8388765;
RA   Little M.H., Williamson K.A., Mannens M., Kelsey A., Gosden C.,
RA   Hastie N.D., van Heyningen V.;
RT   "Evidence that WT1 mutations in Denys-Drash syndrome patients may act
RT   in a dominant-negative fashion.";
RL   Hum. Mol. Genet. 2:259-264(1993).
RN   [19]
RP   VARIANTS DDS TRP-394 AND PRO-398.
RX   MEDLINE=94125627; PubMed=8295405;
RA   Tsuda M., Sakiyama T., Kitagawa T., Watanabe S., Watanabe T.,
RA   Takahashi S., Kawaguchi H., Ito K.;
RT   "Molecular analysis of two Japanese cases of Denys-Drash syndrome.";
RL   J. Inherit. Metab. Dis. 16:876-880(1993).
RN   [20]
RP   VARIANT MESOTHELIOMA GLY-273.
RX   MEDLINE=94004972; PubMed=8401592;
RA   Park S., Schalling M., Bernard A., Maheswaran S., Shipley G.C.,
RA   Roberts D., Fletcher J., Shipman R., Rheinwald J., Demetri G.,
RA   Griffin J., Minden M., Housman D.E., Haber D.A.;
RT   "The Wilms tumour gene WT1 is expressed in murine mesoderm-derived
RT   tissues and mutated in a human mesothelioma.";
RL   Nat. Genet. 4:415-420(1993).
RN   [21]
RP   VARIANT DDS ARG-377.
RX   MEDLINE=94156335; PubMed=8112732;
RA   Nordenskjold A., Friedman E., Anvret M.;
RT   "WT1 mutations in patients with Denys-Drash syndrome: a novel mutation
RT   in exon 8 and paternal allele origin.";
RL   Hum. Genet. 93:115-120(1994).
RN   [22]
RP   VARIANT DDS TYR-373.
RX   MEDLINE=97114281; PubMed=8956030;
RA   Ghahremani M., Chan C.B., Bistritzer T., Aladjem M.M., Tieder M.,
RA   Pelletier J.;
RT   "A novel mutation H373Y in the Wilms' tumor suppressor gene, WT1,
RT   associated with Denys-Drash syndrome.";
RL   Hum. Hered. 46:336-338(1996).
RN   [23]
RP   VARIANTS WT1 SER-181 AND ALA-253.
RX   MEDLINE=97268681; PubMed=9108089; DOI=10.1073/pnas.94.8.3972;
RA   Schumacher V., Schneider S., Figge A., Wildhardt G., Harms D.,
RA   Schmidt D., Weirich A., Ludwig R., Royer-Pokora B.;
RT   "Correlation of germ-line mutations and two-hit inactivation of the
```

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  Query Match             96.0%;  Score 1386;  DB 1;  Length 449;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-77;
  Matches  248;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 61

Qy         69 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 121

Qy        129 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 181

Qy        189 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 241

Qy        249 NLGATLKG 256
              ||||||||
Db        242 NLGATLKG 249
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RESULT 3
WT1_PIG
ID   WT1_PIG         STANDARD;      PRT;   449 AA.
AC   O62651;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Wilms' tumor protein homolog.
GN   Name=WT1;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).
RC   STRAIN=LWD; TISSUE=Kidney;
RX   MEDLINE=98267201; PubMed=9602131; DOI=10.1016/S0378-1119(98)00112-7;
RA   Tsurutani N., Oda H., Nakatsuru Y., Imai Y., Zhang S., Ueno Y.,
RA   Ishikawa T.;
RT   "cDNA cloning and developmental expression of the porcine homologue of
RT   WT1.";
RL   Gene 211:215-220(1998).
CC   -!- FUNCTION: Potential role in transcriptional regulation. Recognizes
CC       and binds to the DNA sequence 5'-CGCCCCCGC-3'.
CC   -!- SUBUNIT: Interacts with ZNF224 via the zinc-finger region.
CC       Interacts with WTAP (By similarity).
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC         Comment=Experimental confirmation may be lacking for some
CC         isoforms;
CC       Name=1;
CC         IsoId=O62651-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=O62651-2; Sequence=VSP_006870, VSP_006871;
CC       Name=3;
CC         IsoId=O62651-3; Sequence=VSP_006870;
CC       Name=4;
CC         IsoId=O62651-4; Sequence=VSP_006871;
CC   -!- DEVELOPMENTAL STAGE: Expressed during kidney development.
CC   -!- SIMILARITY: Belongs to the EGR C2H2-type zinc-finger protein
CC       family.
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CC   -!- SIMILARITY: Contains 4 C2H2-type zinc fingers.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB010969; BAA28147.1; -.
DR   HSSP; P08046; 1F2I.
DR   InterPro; IPR000976; Wilms_tumour.
DR   InterPro; IPR007087; Znf_C2H2.
DR   Pfam; PF02165; WT1; 1.
DR   Pfam; PF00096; zf-C2H2; 4.
DR   PRINTS; PR00049; WILMSTUMOUR.
DR   ProDom; PD000003; Znf_C2H2; 2.
DR   SMART; SM00355; ZnF_C2H2; 4.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
KW   Alternative splicing; Anti-oncogene; DNA-binding; Metal-binding;
KW   Nuclear protein; Repeat; Transcription regulation; Zinc-finger.
FT   DOMAIN       28     83       Pro-rich.
FT   ZN_FING     323    347       C2H2-type 1.
FT   ZN_FING     353    377       C2H2-type 2.
FT   ZN_FING     383    405       C2H2-type 3.
FT   ZN_FING     414    438       C2H2-type 4.
FT   VARSPLIC    249    265       Missing (in isoform 2 and isoform 3).
FT                                /FTId=VSP_006870.
FT   VARSPLIC    407    409       Missing (in isoform 2 and isoform 4).
FT                                /FTId=VSP_006871.
SQ   SEQUENCE   449 AA;  49166 MW;  9C3E557B96F5A7B3 CRC64;

  Query Match             94.7%;  Score 1367;  DB 1;  Length 449;
  Best Local Similarity   98.8%;  Pred. No. 2.8e-76;
  Matches  245;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          9 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 68
              |||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db          2 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAEWAPVLDFAPPGASAYGSLGGPAPPPAPP 61

Qy         69 PPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 128
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db         62 PPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYEPFGPPPPSQAS 121

Qy        129 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 181

Qy        189 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 248
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        182 MGQQGSLGEQQYSVPPPVYGCHTSTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 241

Qy        249 NLGATLKG 256
              ||||||||
Db        242 NLGATLKG 249


RESULT 4
WT1_RAT
ID   WT1_RAT        STANDARD;      PRT;   448 AA.
AC   P49952;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Wilms' tumor protein homolog.
GN   Name=Wt1; Synonyms=Wt-1;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).
RC   STRAIN=Sprague-Dawley; TISSUE=Kidney;
RX   MEDLINE=93046155; PubMed=1330293;
RA   Sharma P.M., Yang X., Bowman M., Roberts V., Sukumar S.;
RT   "Molecular cloning of rat Wilms' tumor complementary DNA and a study
RT   of messenger RNA expression in the urogenital system and the brain.";
RL   Cancer Res. 52:6407-6412(1992).
CC   -!- FUNCTION: Potential role in transcriptional regulation. Recognizes
CC       and binds to the DNA sequence 5'-CGCCCCCGC-3'.
CC   -!- SUBUNIT: Interacts with ZNF224 via the zinc-finger region.
CC       Interacts with WTAP (By similarity).
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC       Name=1;
CC         IsoId=P49952-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=P49952-2; Sequence=VSP_006872, VSP_006873;
CC       Name=3;
CC         IsoId=P49952-3; Sequence=VSP_006872;
CC       Name=4;
CC         IsoId=P49952-4; Sequence=VSP_006873;
CC   -!- TISSUE SPECIFICITY: Kidney.
CC   -!- DEVELOPMENTAL STAGE: Expressed during kidney development.
CC   -!- SIMILARITY: Belongs to the EGR C2H2-type zinc-finger protein
CC       family.
CC   -!- SIMILARITY: Contains 4 C2H2-type zinc fingers.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X69716; CAA49373.1; -.
DR   HSSP; P08046; 1F2I.
DR   TRANSFAC; T02352; -.
DR   RGD; 3974; Wt1.
DR   InterPro; IPR000976; Wilms_tumour.
DR   InterPro; IPR007087; Znf_C2H2.
DR   Pfam; PF02165; WT1; 1.
DR   Pfam; PF00096; zf-C2H2; 4.
DR   PRINTS; PR00049; WILMSTUMOUR.
DR   ProDom; PD000003; Znf_C2H2; 2.
DR   SMART; SM00355; ZnF_C2H2; 4.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
KW   Alternative splicing; Anti-oncogene; DNA-binding; Metal-binding;
KW   Nuclear protein; Repeat; Transcription regulation; Zinc-finger.
FT   DOMAIN       27     82       Pro-rich.
FT   ZN_FING     322    346       C2H2-type 1.
FT   ZN_FING     352    376       C2H2-type 2.
FT   ZN_FING     382    404       C2H2-type 3.
FT   ZN_FING     413    437       C2H2-type 4.
FT   VARSPLIC    249    265       Missing (in isoform 2 and isoform 3).
FT                                /FTId=VSP_006872.
FT   VARSPLIC    407    409       Missing (in isoform 2 and isoform 4).
FT                                /FTId=VSP_006873.
SQ   SEQUENCE   448 AA;  49193 MW;  329AC9AC1FF73F76 CRC64;

  Query Match             92.8%;  Score 1340.5;  DB 1;  Length 448;
  Best Local Similarity   97.2%;  Pred. No. 1.2e-74;
  Matches  241;  Conservative    2;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          9 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 68
              |||||||||||||| |||||||| |||||| |||||||||||||||||||||||||| |
Db          2 GSDVRDLNALLPAVSSLGGGGGCGLPVSGARQWAPVLDFAPPGASAYGSLGGPAPPPA-P 60

Qy         69 PPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 128
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db         61 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTLHFSGQFTGTAGACRYGPFGPPPPSQAS 120
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Qy        129 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 188
              ||||||||||||||||||||:|||||||||||||| ||||||||||||||||||||||||
Db        121 SGQARMFPNAPYLPSCLESQPSIRNQGYSTVTFDGAPSYGHTPSHHAAQFPNHSFKHEDP 180

Qy        189 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 240

Qy        249 NLGATLKG 256
              ||||||||
Db        241 NLGATLKG 248


RESULT 5
WT1_MOUSE
ID   WT1_MOUSE      STANDARD;      PRT;   449 AA.
AC   P22561;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Wilms' tumor protein homolog.
GN   Name=Wt1; Synonyms=Wt-1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).
RX   MEDLINE=91141522; PubMed=1671709;
RA   Buckler A.J., Pelletier J., Haber D.A., Glaser T., Housman D.E.;
RT   "Isolation, characterization, and expression of the murine Wilms'
RT   tumor gene (WT1) during kidney development.";
RL   Mol. Cell. Biol. 11:1707-1712(1991).
CC   -!- FUNCTION: Potential role in transcriptional regulation. Recognizes
CC       and binds to the DNA sequence 5'-CGCCCCCGC-3'.
CC   -!- SUBUNIT: Interacts with ZNF224 via the zinc-finger region.
CC       Interacts with WTAP (By similarity).
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC       Name=1;
CC         IsoId=P22561-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=P22561-2; Sequence=VSP_006868, VSP_006869;
CC       Name=3;
CC         IsoId=P22561-3; Sequence=VSP_006868;
CC       Name=4;
CC         IsoId=P22561-4; Sequence=VSP_006869;
CC   -!- TISSUE SPECIFICITY: Kidney.
CC   -!- DEVELOPMENTAL STAGE: Expressed during kidney development.
CC   -!- SIMILARITY: Belongs to the EGR C2H2-type zinc-finger protein
CC       family.
CC   -!- SIMILARITY: Contains 4 C2H2-type zinc fingers.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M55512; AAA40573.1; -.
DR   HSSP; P08046; 1F2I.
DR   TRANSFAC; T02351; -.
DR   MGD; MGI:98968; Wt1.
DR   GO; GO:0005634; C:nucleus; IDA.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   GO; GO:0001654; P:eye morphogenesis; IMP.
DR   GO; GO:0006357; P:regulation of transcription from Pol II pro. . .; IDA.
DR   InterPro; IPR000976; Wilms_tumour.
DR   InterPro; IPR007087; Znf_C2H2.
DR   Pfam; PF02165; WT1; 1.
DR   Pfam; PF00096; zf-C2H2; 4.
DR   PRINTS; PR00049; WILMSTUMOUR.
DR   ProDom; PD000003; Znf_C2H2; 2.
DR   SMART; SM00355; ZnF_C2H2; 4.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
KW   Alternative splicing; Anti-oncogene; DNA-binding; Metal-binding;
KW   Nuclear protein; Repeat; Transcription regulation; Zinc-finger.
FT   DOMAIN       28     83       Pro-rich.
FT   ZN_FING      323    347      C2H2-type 1.
FT   ZN_FING      353    377      C2H2-type 2.
FT   ZN_FING      383    405      C2H2-type 3.
FT   ZN_FING      414    438      C2H2-type 4.
FT   VARSPLIC     250    266      Missing (in isoform 2 and isoform 3).
FT                                /FTId=VSP_006868.
FT   VARSPLIC     408    410      Missing (in isoform 2 and isoform 4).
FT                                /FTId=VSP_006869.
SQ   SEQUENCE   449 AA;  49246 MW;  962381E9C8D7A380 CRC64;

  Query Match             92.0%;  Score 1329;  DB 1;  Length 449;
  Best Local Similarity   96.8%;  Pred. No. 6e-74;
  Matches  241;  Conservative    1;  Mismatches    5;  Indels    2;  Gaps    2;

Qy          9 GSDVRDLNALLPAVPSL-GGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAP 67
              |||||||||||||| || |||||| |||||| ||||||||||||||||||||||||||||
Db          2 GSDVRDLNALLPAVSSLGGGGGGCGLPVSGARQWAPVLDFAPPGASAYGSLGGPAPPPA- 60

Qy         68 PPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQA 127
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db         61 PPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTLHFSGQFTGTAGACRYGPFGPPPPSQA 120

Qy        128 SSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHED 187
              |||||||||||||||||||| |||||||||||| |||||||||||||||||||||||||
Db        121 SSGQARMFPNAPYLPSCLESQPTIRNQGYSTVTFDGAPSYGHTPSHHAAQFPNHSFKHED 180

Qy        188 PMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQ 247
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQ 240

Qy        248 MNLGATLKG 256
              |||||||||
Db        241 MNLGATLKG 249


RESULT 6
Q9I8A1
ID   Q9I8A1      PRELIMINARY;      PRT;   414 AA.
AC   Q9I8A1;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   WT1(-KTS) protein.
GN   Name=WT1(-KTS);
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RA   Kudo T.;
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB033633; BAA94793.1; -.
DR   HSSP; P08046; 1P47.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000976; Wilms_tumour.
DR   InterPro; IPR007087; Znf_C2H2.
```

```
DR   Pfam; PF02165; WT1; 1.
DR   Pfam; PF00096; zf-C2H2; 4.
DR   PRINTS; PR00049; WILMSTUMOUR.
DR   ProDom; PD000003; Znf_C2H2; 2.
DR   SMART; SM00355; ZnF_C2H2; 4.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
SQ   SEQUENCE   414 AA;  46641 MW;  17EB22F8B428A2EF CRC64;

  Query Match             75.8%;  Score 1094.5;  DB 2;  Length 414;
  Best Local Similarity   81.9%;  Pred. No. 1.3e-59;
  Matches  203;  Conservative   10;  Mismatches   18;  Indels   17;  Gaps    3;

Qy          9 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 68
              |||||||||||||:|||| |   ||:||| |||||||||| ||||| |||||
Db          2 GSDVRDLNALLPSVPSLPGNSNCAMPVSSAAQWAPVLDF-PPGAS-YGSLG--------- 50

Qy         69 PPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 128
                    |||||||||||| |::||||| |||||||||||||||||||||||||| |||||
Db         51 ------PHSFIKQEPSWNGSDPHEEQYLSAFTVHFSGQFTGTAGACRYGPFGAPPPSQPP 104

Qy        129 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 188
              ||||||||  ||||:||||| ||||||| || |||||||||||||||||| |||||||||
Db        105 SGQARMFPQRPYLPNCLESQQAIRNQGYGTVAFDGTPSYGHTPSHHAAQFQNHSFKHEDP 164

Qy        189 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 248
              | || |||:||||||||||||||||:|||||||||||||:|||||||||:|||||||||
Db        165 MSQQPSLGDQQYSVPPPVYGCHTPTDTCTGSQALLLRTPYNSDNLYQMTSRLECMTWNQM 224

Qy        249 NLGATLKG 256
              |||:||||
Db        225 NLGSTLKG 232


RESULT 7
Q9I8A0
ID   Q9I8A0      PRELIMINARY;      PRT;   417 AA.
AC   Q9I8A0;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   WT1(+KTS) protein.
GN   Name=WT1(+KTS);
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RA   Kudo T.;
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB033634; BAA94794.1; -.
DR   HSSP; P08046; 1P47.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000976; Wilms_tumour.
DR   InterPro; IPR007087; Znf_C2H2.
DR   Pfam; PF02165; WT1; 1.
DR   Pfam; PF00096; zf-C2H2; 4.
DR   PRINTS; PR00049; WILMSTUMOUR.
DR   ProDom; PD000003; Znf_C2H2; 2.
DR   SMART; SM00355; ZnF_C2H2; 4.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
SQ   SEQUENCE   417 AA;  46957 MW;  47BBF7F6448E7F6C CRC64;

  Query Match             75.8%;  Score 1094.5;  DB 2;  Length 417;
  Best Local Similarity   81.9%;  Pred. No. 1.3e-59;
  Matches  203;  Conservative   10;  Mismatches   18;  Indels   17;  Gaps    3;

Qy          9 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 68
              |||||||||||||:|||| |   ||:||| |||||||||| ||||| |||||
Db          2 GSDVRDLNALLPSVPSLPGNSNCAMPVSSAAQWAPVLDF-PPGAS-YGSLG--------- 50

Qy         69 PPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 128
                    |||||||||||| |::||||| |||||||||||||||||||||||||| |||||
Db         51 ------PHSFIKQEPSWNGSDPHEEQYLSAFTVHFSGQFTGTAGACRYGPFGAPPPSQPP 104

Qy        129 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 188
              ||||||||  ||||:||||| ||||||| || |||||||||||||||||| |||||||||
Db        105 SGQARMFPQRPYLPNCLESQQAIRNQGYGTVAFDGTPSYGHTPSHHAAQFQNHSFKHEDP 164

Qy        189 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 248
              | || |||:||||||||||||||||:|||||||||||||:|||||||||:|||||||||
Db        165 MSQQPSLGDQQYSVPPPVYGCHTPTDTCTGSQALLLRTPYNSDNLYQMTSRLECMTWNQM 224

Qy        249 NLGATLKG 256
              |||:||||
Db        225 NLGSTLKG 232


RESULT 8
Q91030
ID   Q91030      PRELIMINARY;      PRT;   392 AA.
AC   Q91030;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Chick Wilm's tumour protein (Fragment).
GN   Name=CWT1;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole embryo;
RX   MEDLINE=96068905; PubMed=7478606;
RA   Kent J., Coriat A.M., Sharpe P.T., Hastie N., van Heyningen V.;
RT   "The evolution of WT1 sequence and expression in the vertebrates.";
RL   Oncogene 11:1781-1792(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole embryo;
RA   Kent G.R.L.;
RL   Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; X85731; CAA59736.1; -.
DR   HSSP; Q60980; 1P7A.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   Pfam; PF02165; WT1; 1.
DR   Pfam; PF00096; zf-C2H2; 3.
DR   PRINTS; PR00049; WILMSTUMOUR.
DR   ProDom; PD000003; Znf_C2H2; 2.
DR   SMART; SM00355; ZnF_C2H2; 3.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
FT   NON_TER     392    392
SQ   SEQUENCE   392 AA;  43869 MW;  761F01D350E4EDBF CRC64;

  Query Match             75.5%;  Score 1089.5;  DB 2;  Length 392;
  Best Local Similarity   81.5%;  Pred. No. 2.5e-59;
  Matches  202;  Conservative   11;  Mismatches   18;  Indels   17;  Gaps    3;

Qy          9 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 68
              |||||||||||||:|||| |   ||:||| ||||||||| :||||| |||||
Db          2 GSDVRDLNALLPSVPSLPGNSNCAMPVSSAAQWAPVLD-SPPGAS-YGSLG--------- 50
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Qy          69 PPPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 128
               ||||||||||| |::||||| |||||||||||||||||||||||| |||||
Db          51 ------PHSFIKQEPSWNGSDPHEEQYLSAFTVHFSGQFTGTAGACRYGPFGAPPPSQPP 104

Qy         129 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 188
               |||||||| |||||:||||| ||||||| || |||||||||||||||||| |||||||||
Db         105 SGQARMFPQRPYLPNCLESQQAIRNQGYGTVAFDGTPSYGHTPSHHAAQFQNHSFKHEDP 164

Qy         189 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 248
               | || |||:||||||||||||||||:||||||||||||:|||||||||:|||||||||
Db         165 MSQQPSLGDQQYSVPPPVYGCHTPTDTCTGSQALLLRTPYNSDNLYQMTSRLECMTWNQM 224

Qy         249 NLGATLKG 256
               |||:||||
Db         225 NLGSTLKG 232


RESULT 9
P79958
ID   P79958      PRELIMINARY;      PRT;   407 AA.
AC   P79958;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   WT1 protein.
GN   Name=WT1;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=97074667; PubMed=8917094; DOI=10.1016/0378-1119(96)00143-6;
RA   Semba K., Saito-Ueno R., Takayama G., Kondo M.;
RT   "cDNA clonig and its pronephros-specific expression of the Wilms'
RT   tumor suppressor gene, WT1, from Xenopus laevis.";
RL   Gene 175:167-172(1996).
DR   EMBL; D82051; BAA11522.1; -.
DR   PIR; JC5046; JC5046.
DR   HSSP; P08046; 1P47.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000976; Wilms_tumour.
DR   InterPro; IPR007087; Znf_C2H2.
DR   Pfam; PF02165; WT1; 1.
DR   Pfam; PF00096; zf-C2H2; 4.
DR   PRINTS; PR00049; WILMSTUMOUR.
DR   ProDom; PD000003; Znf_C2H2; 2.
DR   SMART; SM00355; ZnF_C2H2; 4.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
SQ   SEQUENCE   407 AA;  45983 MW;  E2554C658005870C CRC64;

  Query Match             67.3%;  Score 971.5;  DB 2;  Length 407;
  Best Local Similarity   73.7%;  Pred. No. 4.5e-52;
  Matches  182;  Conservative   19;  Mismatches   23;  Indels   23;  Gaps    6;

Qy           9 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 68
               ||||||:| ||| | || |   | :||| ::|||||||| ||||  | ||
Db           2 GSDVRDMN-LLPPVSSLSGNSSCNMPVSNSSQWAPVLDF-PPGA-PYSSL---------- 48

Qy          69 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 128
               |||||||||:|   :|||:||||||||||||||||||||||| | ||||:
Db          49 -----TPHSFIKQEPTW-NPDPHEDQCLSAFTVHFSGQFTGTAGACRYGPFGAPTPSQAT 102

Qy         129 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 188
               :|||||||||||| :||::| ::|||||| | |||||||||||||| ||| |||||||||
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Db         103 TGQARMFPNAPYLSNCLDNQQSMRNQGYSAVAFDGTPSYGHTPSHHTAQFTNHSFKHEDP 162

Qy         189 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 248
               : || |||||||||||||||||||:|||||||||||||:|||||||    ||||||||
Db         163 ISQQTSLGEQQYSVPPPVYGCHTPTDTCTGSQALLLRTPYNSDNLYQM----ECMTWNQM 218

Qy         249 NLGATLK 255
               |||::||
Db         219 NLGSSLK 225


RESULT 10
O42223
ID   O42223      PRELIMINARY;      PRT;   390 AA.
AC   O42223;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Wilms tumor 1 protein.
GN   Name=TWT1;
OS   Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Testudines; Cryptodira; Testudinoidea; Emydidae; Trachemys.
OX   NCBI_TaxID=34903;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Spotila L.D., Hall S.E.;
RL   Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF019779; AAB70832.1; -.
DR   HSSP; P08046; 1P47.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000976; Wilms_tumour.
DR   InterPro; IPR007087; Znf_C2H2.
DR   Pfam; PF02165; WT1; 1.
DR   Pfam; PF00096; zf-C2H2; 3.
DR   PRINTS; PR00049; WILMSTUMOUR.
DR   ProDom; PD000003; Znf_C2H2; 2.
DR   SMART; SM00355; ZnF_C2H2; 4.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
SQ   SEQUENCE   390 AA;  43620 MW;  1C9987435BE927C2 CRC64;

  Query Match             66.3%;  Score 957.5;  DB 2;  Length 390;
  Best Local Similarity   74.2%;  Pred. No. 3.1e-51;
  Matches  184;  Conservative   10;  Mismatches   25;  Indels   29;  Gaps    5;

Qy           9 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 68
               ||||||||||||:| || |   ||:||| |||||||||| ||||| ||||
Db           2 GSDVRDLNALLPSVSSLPGNSNCAMPVSSAAQWAPVLDF-PPGAS-YGSLA--------- 50

Qy          69 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 128
                          ||||||||||  ::|||||||||||||||||||||||||||||| |||:||
Db          51 ------PHSFIKQEPSWNASDPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGAPPPTQAP 104

Qy         129 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 188
               | ||||||| ||||:||||| |||||||||| |||||||||||||||||| |||||||||
Db         105 SSQARMFPNGPYLPNCLESQQAIRNQGYSTVAFDGTPSYGHTPSHHAAQFTNHSFKHEDP 164

Qy         189 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYS-------SDN-----LYQM 236
               : || |||:|||||||||||||||||||||||||||||:       |||      ||
Db         165 ISQQTSLGDQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYNSHATGYESDNHTGPMLYSC 224

Qy         237 TSQLECMT 244
               :|    |
Db         225 GAQYRIHT 232


RESULT 11
Q91657
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ID   Q91657      PRELIMINARY;      PRT;   409 AA.
AC   Q91657;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   WT1.
GN   Name=WT1;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96363858; PubMed=8725280;
RX   DOI=10.1002/(SICI)1097-0177(199606)206:2<131::AID-AJA2>3.3.CO;2-I;
RA   Carroll T.J., Vize P.D.;
RT   "Wilms' tumor suppressor gene is involved in the development of
RT   disparate kidney forms: evidence from expression in the Xenopus
RT   pronephros.";
RL   Dev. Dyn. 206:131-138(1996).
DR   EMBL; U42011; AAB53152.1; -.
DR   HSSP; P08046; 1P47.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   Pfam; PF02165; WT1; 1.
DR   Pfam; PF00096; zf-C2H2; 4.
DR   PRINTS; PR00049; WILMSTUMOUR.
DR   ProDom; PD000003; Znf_C2H2; 2.
DR   SMART; SM00355; ZnF_C2H2; 4.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
SQ   SEQUENCE   409 AA;  46186 MW;  2217FC04612CDE10 CRC64;

  Query Match             65.1%;  Score 940.5;  DB 2;  Length 409;
  Best Local Similarity   71.7%;  Pred. No. 3.6e-50;
  Matches  177;  Conservative   19;  Mismatches   30;  Indels   21;  Gaps    5;

Qy          9 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 68
              ||||||:| ||| | || |    | :||| :||||||||| | |
Db          2 GSDVRDMN-LLPPVSSLSGNSSCNMPVSSSAQWAPVLDF-PRG----------------- 42

Qy         69 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSAFTVHFSGQFTGTAGACRYGPFGPPPPSQAS 128
              |   | |  ||||||:|   :|||:||||||||||||||||||||||||| | ||||:
Db         43 PLQLPDPSLFIKQEPTW-NPDPHEDQCLSAFTVHFSGQFTGTAGACRYGPFGAPTPSQAT 101

Qy        129 SGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFKHEDP 188
              :|||||| ||||| :||::|  :|||||| | |||||||||||| | :|| ||||||||||
Db        102 TGQARMFSNAPYLSNCLDNQQGMRNQGYSAVAFDGTPSYGHTPS-HTSQFTNHSFKHEDP 160

Qy        189 MGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLECMTWNQM 248
              : || ||||||||||||||||||:||||||||||||:||||| |||||:|||||||
Db        161 LSQQTSLGEQQYSVPPPVYGCHTPTDTCTGSQALLLRTPYNSDNLYPMTSQLDCMTWNQM 220

Qy        249 NLGATLK 255
              |||::||
Db        221 NLGSSLK 227


RESULT 12
Q9W611
ID   Q9W611      PRELIMINARY;      PRT;   426 AA.
AC   Q9W611;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   WT1.
OS   Cynops pyrrhogaster (Japanese common newt).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
OX   NCBI_TaxID=8330;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=99081568; PubMed=9865970;
RA   Nakayama Y., Yamamoto T., Matsuda Y., Abe S.-I.;
RT   "Cloning of cDNA for newt WT1 and the differential expression during
RT   spermatogenesis of the Japanese newt, Cynops pyrrhogaster.";
RL   Dev. Growth Differ. 40:599-608(1998).
DR   EMBL; AB013888; BAA76399.1; -.
DR   HSSP; P08046; 1P47.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000976; Wilms_tumour.
DR   InterPro; IPR007087; Znf_C2H2.
DR   Pfam; PF02165; WT1; 1.
DR   Pfam; PF00096; zf-C2H2; 4.
DR   PRINTS; PR00049; WILMSTUMOUR.
DR   ProDom; PD000003; Znf_C2H2; 2.
DR   SMART; SM00355; ZnF_C2H2; 4.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
SQ   SEQUENCE   426 AA;  47590 MW;  46A0B158A9F79C6C CRC64;

  Query Match             64.6%;  Score 933;  DB 2;  Length 426;
  Best Local Similarity   67.5%;  Pred. No. 1.1e-49;
  Matches  172;  Conservative   22;  Mismatches   37;  Indels   24;  Gaps    4;

Qy          9 GSDVRDLNALLPAVPSLGGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAPP 68
              ||||||::|||| | || ||| |::|: | :||||:|||:|   : ||||
Db          2 GSDVRDMSALLPPVSSLAGGGSCSIPMGGGSQWAPMLDFSP--GAPYGSLA--------- 50

Qy         69 PPPPPPPHSFIKQEPSWGGAEPHEEQCLSA-FTVHFSGQFTGTAGACRYGPFGPPP---- 123
                  |||:|||||||||   ||:|||||  ||||| | |||| ||||| || ||
Db         51 ------PHSYIKQEPSWGGGSLHEDQCLSAKVTVHFSSQITGTAEACRYGAFGAPPSSRA 104

Qy        124 --PSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNH 181
                 |||  : | ||| | ||||:|||:  |||||||: : ||| ||||||||| ||| ||
Db        105 PQPSQPPAAQVRMFSNGPYLPNCLENPQAIRNQGYNALAFDGAPSYGHTPSHHVAQFTNH 164

Qy        182 SFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSSDNLYQMTSQLE 241
              |||||||| || || :|||||||||||||||||||||||||:||:||:| ||||| |
Db        165 SFKHEDPMSQQTSLADQQYSVPPPVYGCHTPTDSCTGSQALLLRSPYNSDSLCQMTSQFE 224

Qy        242 CMTWNQMNLGATLKG 256
              ||||||||||:: ||
Db        225 CMTWNQMNLGSSFKG 239


RESULT 13
Q9PUT7
ID   Q9PUT7      PRELIMINARY;      PRT;   419 AA.
AC   Q9PUT7;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Wilms' tumor suppressor.
GN   Name=wt1;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Smith S.I., Down M., Power M., Boyd A.W.;
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF144550; AAF00123.1; -.
DR   HSSP; P08046; 1P47.
DR   ZFIN; ZDB-GENE-980526-558; wt1.
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DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR000976; Wilms_tumour.
DR   InterPro; IPR007087; Znf_C2H2.
DR   Pfam; PF02165; WT1; 1.
DR   Pfam; PF00096; zf-C2H2; 4.
DR   PRINTS; PR00049; WILMSTUMOUR.
DR   ProDom; PD000003; Znf_C2H2; 2.
DR   SMART; SM00355; ZnF_C2H2; 4.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
SQ   SEQUENCE   419 AA;  46925 MW;  606ADFEDA619EECD CRC64;

  Query Match             58.6%;  Score 845.5;  DB 2;  Length 419;
  Best Local Similarity   65.5%;  Pred. No. 2.4e-44;
  Matches  167;  Conservative   17;  Mismatches   42;  Indels   29;  Gaps    9;

Qy          9 GSDVRDLNALLPAVPSL-GGGGGCALPVSGAAQWAPVLDF---APPGASAYGSLGGPAPP 64
              ||||||| ||| || | || | | |||   || |:|||   ||     ||||
Db          2 GSDVRDLNTLLPPVPPLPGGNGNCTLPVSSTPQWPPMLDFHTGAP-----YGSLA----- 51

Qy         65 PAPPPPPPPPPHSFIKQEPSWGGAEPHEE-QC-LSAFTVHFSGQFTGTAGACRYGPFGPP 122
                        |||||||||| |:|||:  | |||||||||||||| |||||| || |
Db         52 ----------QHSFIKQEPSWGTADPHEDPHCGLSAFTVHFSGQFTGT-GACRYGAFGAP 100

Qy        123 PPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHS 182
                ||    | ||| |:||| :|::|| : ||||| || |||  :|||||||  ||||||
Db        101 AASQPPPSQPRMFSNSPYLSNCMDSQSSSRNQGYGTVAFDGASNYGHTPSHHTPQFPNHS 160

Qy        183 FKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPY-SSDNLYQMTSQLE 241
              ||||| : || ::|:||| |||||||||||:|||||||||||| || |||||||| ||||
Db        161 FKHEDSITQQSNMGDQQYPVPPPVYGCHTPSDSCTGSQALLLRNPYNSSDNLYQMASQLE 220

Qy        242 CMTWNQMN-LGATLK 255
              || || :| | :|:|
Db        221 CMGWNPVNSLASTIK 235


RESULT 14
Q90XX6
ID   Q90XX6      PRELIMINARY;      PRT;   417 AA.
AC   Q90XX6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Wilms' tumor suppressor 1b variant.
GN   Name=WT-t1b;
OS   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8022;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21337607; PubMed=11444705; DOI=10.1139/gen-44-3-455;
RA   Brunelli J.P., Robison B.D., Thorgaard G.H.;
RT   "Ancient and recent duplications of the rainbow trout Wilms' tumor
RT   gene.";
RL   Genome 44:455-462(2001).
DR   EMBL; AF334672; AAK52721.1; -.
DR   HSSP; P08046; 1P47.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   Pfam; PF02165; WT1; 1.
DR   Pfam; PF00096; zf-C2H2; 4.
DR   PRINTS; PR00049; WILMSTUMOUR.
DR   ProDom; PD000003; Znf_C2H2; 2.
DR   SMART; SM00355; ZnF_C2H2; 4.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
SQ   SEQUENCE   417 AA;  46557 MW;  5217620CD471D030 CRC64;

  Query Match             56.9%;  Score 822;  DB 2;  Length 417;
  Best Local Similarity   64.5%;  Pred. No. 6.7e-43;
  Matches  165;  Conservative   22;  Mismatches   37;  Indels   32;  Gaps   11;

Qy          9 GSDVRDLNALLPAVPSL-GGGGGCALPVSGAAQWAPVLDF---APPGASAYGSLGGPAPP 64
              |||||||||||| ||:| || | | |||| | || |||||    ||      | ||
Db          2 GSDVRDLNALLPPVPALPGGNGNCTLPVSSAPQWGPVLDFHTGAP-----YSSLA----- 51

Qy         65 PAPPPPPPPPPHSFIKQEPSWGGAEPHEE-QC-LSAFTVHFSGQFTGTAGACRYGPFG-P 121
                        ||||||||||    :| |:  | |||||:|||||||||| |||||| || |
Db         52 ----------PHSFIKQEPSWSSGDPQEDPHCGLSAFTLHFSGQFTGT-GACRYGAFGAP 100

Qy        122 PPPSQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNH 181
              |||||     | ||| ||||| :|:::||: ||||||    |||  :|||||:||::|| :|
Db        101 PPPSQPPPSQPRMFSNAPYLTNCMDTQPSSRNQGYS--AFDGATNYGHTPTHHSSQFLSH 158

Qy        182 SFKHEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPY-SSDNLYQMTSQL 240
              ||| |: : || |:||| |||||||||||:|||||||||||| || |||||||| |||
Db        159 SFKDENSLAQQTSMGEQPYSVPPPVYGCHTPSDSCTGSQALLLRNPYNSSDNLYQMASQL 218

Qy        241 ECMTWNQMN-LGATLK 255
              ||| || :: | :|:|
Db        219 ECMAWNPVSTLASTIK 234


RESULT 15
Q90XX8
ID   Q90XX8      PRELIMINARY;      PRT;   386 AA.
AC   Q90XX8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Wilms' tumor suppressor 1a.
GN   Name=WT-t1a;
OS   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8022;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21337607; PubMed=11444705; DOI=10.1139/gen-44-3-455;
RA   Brunelli J.P., Robison B.D., Thorgaard G.H.;
RT   "Ancient and recent duplications of the rainbow trout Wilms' tumor
RT   gene.";
RL   Genome 44:455-462(2001).
DR   EMBL; AF334670; AAK52719.1; -.
DR   HSSP; P08046; 1P47.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   Pfam; PF02165; WT1; 1.
DR   Pfam; PF00096; zf-C2H2; 4.
DR   PRINTS; PR00049; WILMSTUMOUR.
DR   ProDom; PD000003; Znf_C2H2; 3.
DR   SMART; SM00355; ZnF_C2H2; 4.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
SQ   SEQUENCE   386 AA;  43286 MW;  05622EF7642FC9E5 CRC64;

  Query Match             53.7%;  Score 776;  DB 2;  Length 386;
  Best Local Similarity   66.8%;  Pred. No. 4.1e-40;
  Matches  151;  Conservative   15;  Mismatches   36;  Indels   24;  Gaps    8;

Qy          9 GSDVRDLNALLPAVPSL-GGGGGCALPVSGAAQWAPVLDFAPPGASAYGSLGGPAPPPAP 67
              |||||||||||| |||| || | | |||| | || |||||     : | ||
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Db          2 GSDVRDLNALLPPVPSLSGGNGNCTLPVSSAPQWGPVLDFHT--GTPYSSLA-------- 51

Qy         68 PPPPPPPPHSFIKQEPSWGGAEPHEE-QC-LSAFTVHFSGQFTGTAGACRYGPFG-PPPP 124
                 || |||||||||   :|||:  | ||||||||||||||||| |||||| || ||||
Db         52 -------PHPFIKQEPSWSSGDPHEDPHCGLSAFTVHFSGQFTGT-GACRYGAFGAPPPP 103

Qy        125 SQASSGQARMFPNAPYLPSCLESQPAIRNQGYSTVTFDGTPSYGHTPSHHAAQFPNHSFK 184
              ||     | ||| ||||| :|:::||  ||||||   |||| :|||||:||::||||||||
Db        104 SQPPPSQPRMFSNAPYLTNCMDTQPPSRNQGYS--AFDGTTNYGHTPTHHSSQFPNHSFK 161

Qy        185 HEDPMGQQGSLGEQQYSVPPPVYGCHTPTDSCTGSQALLLRTPYSS 230
              ||| : || |:||||| ||||||||||:||| |||||||| ||:|
Db        162 HEDSLAQQTSMGEQQYPVPPPVYGCHTPSDSCAGSQALLLRNPYNS 207
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Search completed: May 10, 2005, 18:44:48
Job time : 175 secs